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From: Shukla, Ram  
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SEQ ID NO 1  
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Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
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TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



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QY 120 slyAspLysValGluPheTyrArgLysLeuHisAlaVal 133
Db 42 CAAAGCAAGTGGATTCTACAGAAACTGCATGCTGG 3

RESULT 14
US-10-290-078-20
; Sequence 20, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692 or 58874
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1014)
US-10-290-078-20

Alignment Scores:
Pred. No.: 7,44e-12 Length: 1014
Score: 250.00 Matches: 68
Percent Similarity: 48.71% Conservative: 83
Best Local Similarity: 21.94% Mismatches: 131
Query Match: 15.70% Indels: 28
DB: 15 Gaps: 11

US-10-055-106c-2 (1-305) x US-10-290-078-20 (1-1014)

QY 3 GlyHisAsnThrSerArgAsnSerGlyCys-----AppProIleValThrPro 18
Db 13 GGAATCTGACAGTATCTCTCCACATGCCATGACATGATTTGATGACTTCGCAATCAA 72

QY 19 HisLeuIleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIle 38
Db 73 GTGATTCCACTTGACTGATGATCTGTGTAGGCTCTTGGCAATGGCTTTGTG 132

QY 39 LeuPheLeuLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
Db 133 CTCTATGCTCTCATAAAAACCTATCACAGAAGTCCAGCCTTCCAAAGTATACATGATTAAT 192

QY 58 LeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIle 77
Db 193 TTAGCAGTAGCAGATCTACTTTGTGTGTCACATGCTCTCCGTGGTCTATATGTT 252

QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 253 CACAAGGCAATTTGGCTCTTTGGTGAATCTTTGTGCGCCCTCAGCAGCCTTCTGTTGAT 312

QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle 116
Db 313 GTCACCTCTATGTAGCATCTCTTTATGACAGCC-----ATAGAGC 354

QY 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
Db 355 TTTTTCGGTGTGATTCGAATTTGTTCCAGTCCAGACATTAATTTGGTTACACAGAAA 414

QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValValProLeu 150
Db 415 AAGCCAGGTTGTGTGTAGTATTTGGATTTTGGATTTTGACCATTTCTCCATTT 474

QY 151 ValValSerArgTyrGlyIleHisGluLeuTyrAsnGluGluHisCysPhePheHis 170
Db 475 CTAATGGCCAAA---CCACAAAAGATGAGAAAATATATACCAAGTGTCTTTGAGCCCCCA 531

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QY 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
Db 532 CAAAGCAATCAAACTAAATAATCATGTTTGGTCTGTGATTTGTCATTTGGTTGGC 591

QY 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
Db 592 TTATCATCCCTTTTGTATTATATATCTGTGTACACATGATCATTTTGCCTTACTA 651

QY 208 ValGlnLysLeuArgHisSerLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
Db 652 AAAAATCAATCAAAAAATCTGCAAGTCATAAAAGGCTATAGNATGATC----- 705

QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
Db 706 ATGTCGTGACCGCTGCTCTTTTGTAGTCTGATGTCATGTCATATCAATCAAGTACCAT 765

QY 248 TyrLeuAsnValVal---ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsn 266
Db 766 CACCTTCATTTTACACAAATCAAACTAAACCTGTGATTCCTTCTAGNATCAGAG 825

QY 267 GluIlePheLeuSerValThrAlaIleSer-----CysTyrAspLeuLeuPhe 283
Db 826 TCGTGTGTCATTAACCTGTCTGTGCTGATCCAAATTTGTCCTTGGACCTCTCTATAT 885

QY 284 ValPheGlyGlySerHisTrpPheLysGln 293
Db 886 TCTTTTCTGGGGTAACCTTTAGGAAAGG 915

RESULT 15
US-10-400-991-7
; Sequence 7, Application US/10400991
; Publication No. US20030224417A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Hunter, John J.
; APPLICANT: White, David
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: 14400, 2838, 14618, 15334, 14274, 32164,
; TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 18405, 32705, 23224,
; TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN-TRANSMEMBRANE
; TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS
; FILE REFERENCE: MPI03-0240NMIM
; CURRENT APPLICATION NUMBER: US/10/400,991
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 10/190,469
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 09/439,159
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/137,063
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 10/167,192
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/420,187
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 09/173,869
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 10/339,056
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 09/377,429
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 09/136,726
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: US 09/911,583
; PRIOR FILING DATE: 2001-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0

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; LENGTH: 810
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-366-504-1

Alignment Scores:
Pred. No.: 2,896-87 Length: 810
Score: 1,441.00 Matches: 219
Percent Similarity: 89.55% Conservative: 21
Best Local Similarity: 81.72% Mismatches: 28
Query Match: 71.67% Indels: 0
DB: 15 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-366-504-1 (1-810)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 1 ATGGATGGATATAATACCTCTGAGATTCCTCTGTGACCTATATCTGCACACCACTTA 60
QY 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ACATCGATTACTTCTAGTGTCTATGGAGGACTGTAGGCTCATCTCCATCCCTGTTTC 120
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 121 TTCTGGTGAATGAACCTACCTCTCAGTGACCACTGCTGTCTATCAACCTCGTGGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 181 GTTCATGGGGTCTTCTCTACTGACGGTGGCTTTCGGCTTGCCATCTCATCAAGGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGGACGTTGATATACCTCTCTGCAATTTGTGAGTGCCATGTATACATATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 301 CTCACGTTCTCTTCTACGTGGTGATAGTACTAGTATCATCAGATACCTCATCTTCTCAAGCGT 360
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 361 AGAGCAAGATAGATTTCTATAGAAATTCATGACGTTGCTGCAAGTTCTGCCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 CTCTCTGGTATTTGTTATTTGTGTCCTTGTGCTTCTCAGTATGGAATACCGAAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGCAACAGTCTTTAGATTCATTAAGAACTTGCCATGATCTGTGCGAGTT 540
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCAACTATATATAGTCAATTTGTGTATAGCTGTTCGCTGTGATTTCTTGGGTTTCCAG 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATTTGTCATGGTGGGAGTTTCGCCACTCTCTTACTATCCCAACAGGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCTGGGCACACTGAAATCTTTCTTTATAGGTATCATTTATTTGTTTCTTCTCC 720
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTCTCTCAGATTTTATTTACTTGTATGTTGTGGCACCATCCCAAGAGCTGAAAC 780
QY 261 LysValAlaPheTyrAsnGluIle 268
Db 781 AAGTTGATTTTACATGAATC 804

RESULT 13
US-09-782-974C-21/c
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; Sequence 21, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-21

Alignment Scores:
Pred. No.: 3,77e-48 Length: 447
Score: 674.00 Matches: 133
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 0
Query Match: 42.34% Indels: 1
DB: 10 Gaps: 0

US-10-055-106C-2 (1-305) x US-09-782-974C-21 (1-447)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 402 ATGCTGTGGCCAAATACCTCTCAGGAATTCCTCTTGGATCTCTAGTGACACCCACTTA 343
QY 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 342 ATCACCTCTACTTCTATAGTCTTATTGGCGGGCTGGTGGTGTCTATTCTCTTTC 283
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 282 CTCCTCGTGGTAAATGAACACCCGGTCAGTACCCACCATGGCGGTCATTAACTTGGTGTG 223
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 222 GTCCACAGCGTTTCTCTGACAGTGCAATTCGTTGACCTACTCTCATCAAGAAGACT 163
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 162 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATCTGTCACATCCACATGTAC 103
QY 101 LeuThr-PheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 102 CTCACGGTCTCTTCTTCTATGTTGGTGTATCTGGTTCACAGATACCTCATCTTCTTCAAGT 43
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Db 565 ATCACTATATAGTACATCTTTTGTGCATAGCGCTTGTGTGATCTGTGTCTTCCAG 624  
 Qy 201 ValPheIleIleMetLeuValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 Db 625 GTCTTCATCATATGTTGATGTGAGAGCTACGCCATCTTTACTATCCACAGGAG 684  
 Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
 Db 685 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCATCTTGTGTTTCTCTCC 744  
 Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260  
 Db 745 TACCACTTCTTAGGATCTATCTACTTGAATGTGACCATCTCCATCCCTGTAGCAGC 804  
 Qy 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 Db 805 AAGTTGTCATTTTATAACGAATCTCTTGAAGTGAACAGCAATTAGCTGTCTATGATTG 864  
 Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
 Db 865 CTCTCTCTTTGTCTTTGGGGAAGCCATTGTTTAAAGCAAAAGATATTGCTTATGGAAT 924  
 Qy 301 CysValLeuCysArg 305  
 Db 925 TGTGTTTTGTGCCGT 939

## RESULT 11

US-10-085-233B-1

; Sequence 1, Application US/10085233B

; Publication No. US20030087249A1

; GENERAL INFORMATION:

; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA

; TITLE OF INVENTION: 93870. A HUMAN G-PROTEIN COUPLED

; FILE OF INVENTION: RECEPTOR AND USES THEREFOR

; FILE REFERENCE: MEI2001-021P1RCP1M

; CURRENT APPLICATION NUMBER: US/10/085,233B

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: 60/272,677

; PRIOR FILING DATE: 2001-03-01

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1684

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (147)...(1085)

; OTHER INFORMATION: n at position 1384 can be any

; OTHER INFORMATION: nucleotide

US-10-085-233B-1

## Alignment Scores:

Pred. No.:	1 58e-124	Length:	1684
Score:	1587.00	Matches:	304
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.67%	Mismatches:	0
Query Match:	99.69%	Indels:	0
DB:	15	Gaps:	0

US-10-055-106c-2 (1-305) x US-10-085-233B-1 (1-1684)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
 Db 171 ATGCTGGGCACAAATACCTCCAGAAATCTCTTGGGATCCCTATAGTACACCCCACTTA 230  
 Qy 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
 Db 231 ATCAGGCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTCTCATTTCCATTTCTTC 290  
 Qy 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
 Db 291 CTCTCGTGAATAATGAACCCCGTCAGTGACCACCATGGCGGTCTTAATTAATTTGGTGGTG 350

Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleLeuLysLysLeuThr 80  
 Db 351 GTCCACAGCGTTTTTCTGCTGACAGTGCCTATTTGCTTGACCTACCTACCTCATCAAGAGACT 410  
 Qy 81 TrpMetPheGlyLeuProPheCysLeuPheValSerAlaMetLeuHisIleHisMetTyr 100  
 Db 411 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGACATCCACATGTAC 470  
 Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuPhePheCys 120  
 Db 471 CTCAGTTCTCTATTTCTATGTGTGATCTCTGTCACCAAGATACCTCATCTCTTCAAGTGC 530  
 Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140  
 Db 531 AAAGACAAAGTGGAAATCTACAGAAACTGTCATGCTGTGCTGCCAGTGTGGCATGTGG 590  
 Qy 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
 Db 591 ACGTGTGTGATTTGTCATTTGTTACCCCTGTTCTCTCCCGGTATGGAATCCATGAGAA 650  
 Qy 161 TyrAsnGlnGluHisCysPhePheHisLysGlnLeuAlaTyrThrTyrValIleVal 180  
 Db 651 TACAATGAGGAGCAGCTGTTTAAATTTTCAACAAGAGCTTGTCTTACACATATGTGAAAATC 710  
 Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
 Db 711 ATCACTATATCATAGTACATTTTGTCTATAGCCGTTGCTGTGATCTGTGTTCTTCCAG 770  
 Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 Db 771 GTCTTCATCATTTATGTTGATGTTGTCAGAAAGTACGCCACTCTTTACTATCCACAGAG 830  
 Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
 Db 831 TCTGGGCTCAGCTGAAACCACTATTTTATAGGGTCACTCTTGTGTTTCTTCTTCCC 890  
 Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
 Db 891 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCGTAGCAGC 950  
 Qy 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 Db 951 AAGTTGCAATTTTATAACGAATCTTCTTGTAGTGTAAAGCAATAGCTATGATTTG 1010  
 Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
 Db 1011 CTCTCTTTGTTCTTGGGGGAGCCATTTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 1070  
 Qy 301 CysValLeuCysArg 305  
 Db 1071 TGTGTTTTGTGCCGT 1085

## RESULT 12

US-10-366-504-1

; Sequence 1, Application US/10366504

; Publication No. US20030166008A1

; GENERAL INFORMATION:

; APPLICANT: Bishindirelo, Haifeng

; APPLICANT: Dressler, Holly

; APPLICANT: Cai, Jidong

; APPLICANT: Wright, Paul

; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH

; FILE REFERENCE: USAV2002/0002 USNP

; CURRENT APPLICATION NUMBER: US/10/366,504

; CURRENT FILING DATE: 2003-02-13

; PRIOR APPLICATION NUMBER: US 60/356,686

; PRIOR FILING DATE: 2002-02-14

; PRIOR APPLICATION NUMBER: GB 0219574.1

; PRIOR FILING DATE: 2002-08-22

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

Alignment Scores:		1.58e-122	Length:	113306
Pred. No.:	1592.00	Matches:	305	
Score:	100.00%	Conservative:	0	
Percent Similarity:	100.00%	Mismatches:	0	
Best Local Similarity:	100.00%	Indels:	0	
Query Match:	16	Gaps:	0	
DB:				
US-10-055-106C-2 (1-305) x US-10-292-798-1007 (1-113306)				
QY	1	MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu	20	
DB	11540	ATGCCTGGCCACATACCTCCAGGAATTCCTCTGGATCCTATAGTGCACACCCCACTTA	11599	
QY	21	IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe	40	
DB	11600	ATCAGCCTCTACTTCATAGTGCCTATTGGCGGGTGGTGGTGCATTCCATTCCTTTTC	11659	
QY	41	LeuLeuValIysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal	60	
DB	11660	CTCCTGTGGAATGAACACCCCGTCACTGACACCACTGCGGTCACTTAATTCCTGGTG	11719	
QY	61	ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuIleLysLysThr	80	
DB	11720	GTCCACAGCGTTTCTCTGCTGACAGTCCCAATTCGCTTGACCTACCTCATCAAGAGACT	11779	
QY	81	TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr	100	
DB	11780	TGGATGTTTGGCTGCGCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC	11839	
QY	101	LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleuIlePhePheLysCys	120	
DB	11840	CTCAGCTTCTCTATCTATGTGTGATCCTGTCACCAAGTACCTCATCTTCTTCAAGTGC	11899	
QY	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr	140	
DB	11900	AAACAAAGTGAATTTCTACAGAAACTGCATGCTGTGGCTGCATGTGCGCATGTGG	11959	
QY	141	ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu	160	
DB	11960	ACGTGTGTGATGTCATTTGTGTGATCCCTGCTGCTCCCGTATGGAATCCATGAGAA	12019	
QY	161	TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIysIle	180	
DB	12020	TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTGTACACATATGTGAATC	12079	
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln	200	
DB	12080	ATCAACTATATGATGATCATTTTGTATAGCCGTGCTGTGATTCCTGTGCTTCCAG	12139	
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220	
DB	12140	GTCTTCATCATATGATGTGATGGTGCAGAAAGTACGCCACTCTTTTACTATCCACAGAG	12199	
QY	221	PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro	240	
DB	12200	TTCTGGGCTCAGCTGAAAAAACCCTATTTTATAGGGGTCACTCTTGTGTTCTTCTCC	12259	
QY	241	TyrGlnPhePheArgIleTyrTyrIleuAsnValValThrHisSerAsnAlaCysAsnSer	260	
DB	12260	TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCTGTAAACGC	12319	
QY	261	LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu	280	
DB	12320	AAGGTGTGATTTTATACGAATCTTCTTGTAGTGTACAGCAATTAGCTGTATGATTG	12379	
QY	281	LeuLeuPheValPheGlyCysHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn	300	
DB	12380	CTTCTCTTGTCTTGGGGAAGCCATTCGTTTAAAGCAAAAGATAATTTGGCTTATGAAAT	12439	
QY	301	CysValLeuCysArg	305	
DB	12440	TGTGTTTGTGCGGT	12454	

PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 09/714,449  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 60/198,568  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: 60/166,071  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: 60/166,678  
PRIOR FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: 60/173,396  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/184,129  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: 60/185,421  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/185,554  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/186,530  
PRIOR FILING DATE: 2000-03-02  
Remaining prior application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 81  
LENGTH: 2525  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-782-974C-81

Alignment Scores:  
Pred. No.: 1,02e-124 Length: 2525  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 10

US-10-055-106C-2 (1-305) x US-09-782-974C-81 (1-2525)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
DB 27 ATGCCTGGCCACAAATACCTCCAGCAATTCCTCTGGGATCCTATAGTGACACCCCACTTA 86  
QY 21 IleSerLeuThrPheLeuValIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 87 ATCAGCCTCTACTTCATAGTGTATTTGGGGGCTGGTGGTGCATTTCCTTCCTTTTC 146  
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
DB 147 CTCTGGTGAANTGACACCCCGTCAGTGACACCACTGGCGGTCAATTAATTTGGTGGTG 206  
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrIleLeuLeuIysThr 80  
DB 207 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTTCGCTTGACCTACCTCATCAAGAGACT 266  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 267 TGGATGTTGGGTGGCCCTTCTGCATAATTGTGAGTGCCATGTGTGCACATCCACATGTAC 326  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuPhePheLysCys 120  
DB 327 CTCACGTTCTCTATTCTATGTGGTGATCCTGGTCACCAGATPACCTCATCTCTTCAAGTGC 386  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAsnLeuMetTyr 140  
DB 387 AAAGACAAAGTGAATTTCTACAGAAACTCATGCTGTGGCTGCCAGTGTGCTGATGTGG 446  
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
DB 447 ACGTGTGTGATTTGTCATTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 506  
QY 161 TyrAsnGluHisCysPheLysPheHisGlyLeuAlaTyrThrTyrValIle 180  
DB 507 TACAATGAGGAGCACTGTTTTAAATTTTCAAAAGAGCTTCTGTACACATATGTGAATTC 566

QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
DB 567 ATCACTATATGATGATGATTTTGTGATAGCCGTGCTGTGATTCCTGTTGGTCTTCCAG 626  
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
DB 627 GTCTTCATCATTTATGTTGATGGTGACAGCTACGCCACTCTTTTACTATATCCCAAGGAG 686  
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
DB 687 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC 746  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
DB 747 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 805  
QY 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
DB 807 AAGGTTGCATTTTATAACGAAATCTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 866  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
DB 867 CTCTCTCTTGTCTTTGGGGAGCAATGGTTTAAAGCAAGATAATTGCTTATGGAAT 926  
QY 301 CysValLeuCysArg 305  
DB 927 TGTGTTTTGTGCCGT 941

RESULT 9  
US-10-292-798-1007  
Sequence 1007, Application US/10292798  
Publication No. US20030235833A1  
GENERAL INFORMATION:  
APPLICANT: SUWA, MAKIKO  
APPLICANT: ASAI, KIYOSHI  
APPLICANT: AKIYAMA, YUTAKA  
APPLICANT: ABURATANI, HIROUKI  
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
FILE REFERENCE: 084335/166  
CURRENT APPLICATION NUMBER: US/10/292,798  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 10/017,161  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: JP 2001-246789  
PRIOR FILING DATE: 2001-06-18  
NUMBER OF SEQ ID NOS: 2070  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1007  
LENGTH: 113306  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: source  
LOCATION: (1) .. (113306)  
FEATURE: (1) .. (113306)  
NAME/KEY: CDS  
LOCATION: (201) .. (207)  
FEATURE: CDS  
LOCATION: (11526) .. (12452)  
NAME/KEY: CDS  
LOCATION: (37954) .. (38097)  
FEATURE: CDS  
LOCATION: (98732) .. (98784)  
NAME/KEY: CDS  
LOCATION: (112891) .. (113106)  
US-10-292-798-1007



ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human TGR343  
US-10-188-405-9

Alignment Scores:

Pred. No.: 2,69e-125 Length: 918  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-188-405-9 (1-918)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
DB 1 ATGCCTGGCCCAATACCTCCAGGAATTCCTTGGCATCCTATAGTGACACCCACTTA 60  
QY 21 IleSerLeuTyrPheIleValValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGTCATTTCCTTTTC 120  
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
DB 121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCACTGGCGGTCAATTAACCTTGGTG 180  
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80  
DB 181 GTCCACAGCGTTTCTGTGACAGTGGCCATTTCCGCTTGACCTACCTCATCAAGAAGACT 240  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 241 TGGATGTTTGGGCTGCCCTCTCGCAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
DB 301 CTCACGTTCTATCTATGTGTGATCCTCGTCACAGATACCTCATCTTCTCAAGTGC 360  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140  
DB 361 AAAGCAAAAGTGGAAATTCACAGAAATGCGATGCTGGCTGCCAGTGGCATGTGG 420  
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
DB 421 AGCTGGTGATGTCTATCTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480  
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
DB 481 TACAATGAGGAGCAGCTGTTTAAATTCACAAAGAGCTTGGCTTACACATATGTGAATTC 540  
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
DB 541 ATCACTATATAGTAGTCAATTTTGTATAGCGGTGTGTGTATCTGTGTCTTCCAG 600  
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
DB 601 GTCTTCATCATTTATGTTGTTGTCAGAAAGTACGCCACTCTTTATATATCCACAGGAG 660  
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
DB 661 TTCGGGCTCAGCTGAAACCACTATTTTATAGGGGTATCTGTTGTTTCCCTTCC 720  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260  
DB 721 TACCAGTCTTTTAGGATCTATTAATCTTGAATGTTGTGACGCATTTCCAAATGCCGTGAACAGC 780  
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
DB 781 AAGGTGTCATTTTATACGGAATCTTCTGAGGTGAACGAATTAAGTGTCTATGATTG 840  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300

DB 841 CTTCTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900  
QY 301 CysValLeuCysArg 305  
DB 901 TGTGTTTTGTGGGT 915  
RESULT 6  
US-10-293-171-1  
; Sequence 1, Application US/102931171  
; Publication No. US20030138418A1  
; GENERAL INFORMATION:  
; APPLICANT: Eishingdrelo, Haifeng  
; APPLICANT: Cai, Jidong  
; APPLICANT: Gassenhuber, Johann  
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH  
; FILE REFERENCE: USAV2001/0158 US NP  
; CURRENT APPLICATION NUMBER: US/10/293,171  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US60/354,150  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1040  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-293-171-1

Alignment Scores: 3,16e-125 Length: 1040  
Pred. No.: 1592.00 Matches: 305  
Score: 1592.00 Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 15

US-10-055-106C-2 (1-305) x US-10-293-171-1 (1-1040)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
DB 1 ATGCCTGGCCCAATACCTCCAGGAATTCCTTGGCATCCTATAGTGACACCCACTTA 60  
QY 21 IleSerLeuTyrPheIleValValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGTCATTTCCTTTTC 120  
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
DB 121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCACTGGCGGTCAATTAACCTTGGTG 180  
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80  
DB 181 GTCCACAGCGTTTCTGTGACAGTGGCCATTTCCGCTTGACCTACCTCATCAAGAAGACT 240  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 241 TGGATGTTTGGGCTGCCCTCTCGCAATTTGAGTGCCATGCTGTGCACATCCACATGTAC 300  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
DB 301 CTCAGTTCCTTATCTATGTGTGATCCTGTGTACAGATACCTCATCTTCTCAAGTGC 360  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140  
DB 361 AAAGCAAAAGTGGAAATTCACAGAAATGCGATGCTGGCTGCCAGTGGCATGTGG 420  
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
DB 421 ACGTGGTGATGTCTATGTTGTTGCTTCCCGGTATGGAATCCATGAGGAA 480  
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
DB 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGGCTTACACATATGTGAATTC 540

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Db      541 ATCACTATATAGTATGCTATTTTGTATAGCGGTTGCTGATTCGTGGTCTTCAG 600
Qy      201 ValPheLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db      601 GTCCTCATCATATGTTGATGTGAGGAGGCTACGCCACTCTTTACTATCCACAGGAG 660
Qy      221 PheTrpAlaGlnLeuLysAsnLeuPhePheLeuGlyValLeuValCysPheLeuPro 240
Db      661 TTCCTGGGCTCAGTGAACCACTATTTTATAGGGTCACTCTGTTGTTGTTCTTCTCC 720
Qy      241 TyrGlnPhePheArgLeuTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db      721 TACCACTCTTTAGGATCTATTACTTTGAATGTGTGACGCAATTAAGCTGCTATGATTG 840
Qy      261 LysValAlaPheTyrAsnGlnLysLeuSerValThrAlaLeuSerCysTyrAspLeu 280
Db      781 AAGTTTGCATTTTATACGAATCTTCTTGAGTGTAAACGAATTAAGCTGCTATGATTG 840
Qy      281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysValLeuLeuLeuTrpAsn 300
Db      841 CTTCTCTTTGCTTTTGGGGAGGCAATGTTTAAAGCAAAAGATATTTGGCTTATGGAAT 900
Qy      301 CysValLeuCysArg 305
Db      901 TGTGTTTGTGCCGT 915

RESULT 4
US-10-055-106C-1
; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Harland, Lee
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-055-106C-1

Alignment Scores:
Pred. No.:      2,68e-125      Length:      918
Score:          1592.00      Matches:      305
Percent Similarity: 100.00%      Conservatives: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              13          Gaps: 0

US-10-055-106C-2 (1-305) x US-10-055-106C-1 (1-918)
Qy      1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db      1 ATGCTGGGCCAATACCTCCAGGAATTCCTCTGGCATCTCTATAGTACACCCCACTTA 60
Qy      21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db      61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGCTGTGGTGTGTCATTTCATTTCTTTTC 120
Qy      41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db      121 CTCCTGGTGAATAATGAACCCCGTCACTGACCACTTGGCGGTCAATTAATTTGGTGGTG 180
Qy      61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuLeuLysLysThr 80

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Db      181 GTCCACAGCCGTTTTTCTGTGACAGTGCCTATTTGCTTGCCTACCTCATCAAGAAGACT 240
Qy      81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db      241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTATC 300
Qy      101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db      301 CTCACGTTCTCTATTCATATGGGTGATCCTGCTCACCAGATACCTCATCTTCTTCAAGTGC 360
Qy      121 LysAspLysValGlnPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db      361 AAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGCTGCCAGTGTGTCATGTGG 420
Qy      141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGlnGlu 160
Db      421 ACGTGTGTGATTGTGATTTGGGTACCCCTGTTGTCTCCCGTATGGATCCATCCATGAGAA 480
Qy      161 TyrAsnGlnLysHisCysPheLysPheHisLysGlnLeuAlaTyrThrTyrValLysIle 180
Db      481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540
Qy      181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
Db      541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTCCTGTGCTTTCAG 600
Qy      201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db      601 GCTTTCATCATATGTTGATGTGTCAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 660
Qy      221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db      661 TTCCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTGTTGTTGTTCTCTCC 720
Qy      241 TyrGlnPhePheArgLeuTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db      721 TACCAGTCTTTTAGATCTATTAAGTGTGTGACGCAATTCATCCATGCCGTATGATTG 780
Qy      261 LysValAlaPheTyrAsnGlnLysLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db      781 AAGTTTGCATTTTATACGAATCTTCTTGTAGTGTAAACGAATTAAGCAAAAGATATTTGGCTTATGGAAT 840
Qy      281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db      841 CTTCTCTTTGCTTTTGGGGAGGCAATTTGTTTAAAGCAAAAGATATTTGGCTTATGGAAT 900
Qy      301 CysValLeuCysArg 305
Db      901 TGTGTTTGTGCCGT 915

RESULT 5
US-10-188-405-9
; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1el Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA

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Pred. No.: 2.68e-125 Length: 918  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-055-106C-2 (1-305) x US-09-995-325-3 (1-918)

```
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTGGATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGTCAATTCCTTTTC 120
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAATGAACCCGGTCAGTGACCCATGGCGGTCAATTAAGTTGGTGGTG 180
QY 61 ValHisSerValPheLeuThrValProPheArgLeuThrTyLeuIleLysLeuThr 80
DB 181 GTCCACAGCGTTCCTGCTACAGTGCCATTCGCTTGACCTACCTACCTCAAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysIlePheValSerAlaValMetLeuHisMetTy 100
DB 241 TGGATGTTTGGGCTGCCCTCTCGAAATTTGTGAGTGCCTGCTGCACATCCATGTAC 300
QY 101 LeuThrPheLeuPheTyValIleLeuValThrArgTyLeuIlePhePheLysCys 120
DB 301 CTCAGTTTCCTATCTATGTTGGTATCTGCTGCTACCAAGAGCTGCTTCAAGTGC 360
QY 121 LysAspLysValGluPheTyArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
DB 361 AAAGACAAAGTGGAAATCTACAGAAATCTGATGCTGCTGCGGCTGCGCATGTGG 420
QY 141 ThrLeuValIleValIleValValProLeuValValSerArgTyGlyIleHisGluGlu 160
DB 421 ACGCTGGTGAATGTCATTTGGTACCCTGTTGCTCCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyThrTyValLysIle 180
DB 481 TACAATGAGGAGCAGCTGTTTAAATTTTACAAAGAGCTGCTTACACATATGTGAAATC 540
QY 181 IleAsnTyMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 541 ATCACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTGTTGGTCTCCAG 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 601 GTCTTCATCATTTATGTTGATGTCAGAAAGCTAGCCCACTCTTTTACTATCCCAAGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 661 TTCTGGGCTACGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCCC 720
QY 241 TyrGlnPhePheArgIleTyTyLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 721 TACCAGTTCTTTAGGATCTATTAATCTGAAATGTTGACGCAATCCAAATGCTGTAAACAGC 780
QY 261 LysValAlaPheTyAsnGluIlePheLeuSerValThrAlaIleSerCysTyAspLeu 280
DB 781 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACGCAATAGCTGTATGATTTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
DB 841 CTTCCTCTTTGCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
DB 901 TGTGTTTGTGCCGT 915
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## RESULT 3

US-10-297-908A-2  
Sequence 2, Application US/10297908A  
Publication No. US20040029793A1

## GENERAL INFORMATION:

APPLICANT: MORIYA, Takeo  
APPLICANT: ITO, Takahashi  
APPLICANT: SHINTANI, Yasushi  
APPLICANT: MIYAJIMA, No. US20040029793A1  
TITLE OF INVENTION: US20040029793A1 G Protein-Coupled Receptor Protein and its  
FILE REFERENCE: 2737 USOP  
CURRENT APPLICATION NUMBER: US/10/297,908A  
CURRENT FILING DATE: 2002-12-11  
PRIOR APPLICATION NUMBER: PCT/JP01/05061  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: JP 2000-184596  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: JP 2000-223887  
PRIOR FILING DATE: 2000-07-19  
NUMBER OF SEQ ID NOS: 7  
SEQ ID NO 2  
LENGTH: 918  
TYPE: DNA  
ORGANISM: Human  
US-10-297-908A-2

## Alignment Scores:

Pred. No.: 2.68e-125 Length: 918  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-297-908A-2 (1-918)

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QY 21 IleSerLeuTyPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGTCAATTCCTTTTC 120
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAATGAACCCGGTCAGTGACCCATGGCGGTCAATTAAGTTGGTGGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyLeuIleLysLysThr 80
DB 181 GTCCACAGCGTTCCTGCTGACAGTGCCATTCGCTTGACCTACCTCAAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
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QY 101 LeuThrPheLeuPheTyValValIleLeuValThrArgTyLeuIlePhePheLysCys 120
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QY 121 LysAspLysValGluPheTyArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
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DB 421 ACGCTGGTGAATGTCATTTGGTACCCTGTTGCTCCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyThrTyValLysIle 180
DB 481 TACAATGAGGAGCAGCTGTTTAAATTTTACAAAGAGCTGCTTACACATATGTGAAATC 540
QY 181 IleAsnTyMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
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, PRIOR APPLICATION NUMBER: 60/270,286
, PRIOR FILING DATE: 2001-02-20
, PRIOR APPLICATION NUMBER: 60/282,365
, PRIOR FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: 60/270,266
, PRIOR FILING DATE: 2001-02-20
, PRIOR APPLICATION NUMBER: 60/282,032
, PRIOR FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: 60/282,358
, PRIOR FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: 60/282,356
, PRIOR FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: 60/290,917
, PRIOR FILING DATE: 2001-05-14
, PRIOR APPLICATION NUMBER: 60/309,208
, PRIOR FILING DATE: 2001-07-31
, NUMBER OF SEQ ID NOS: 67
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 3
, LENGTH: 918
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-995-225-3

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RESULT 2
US-09-995-225-3
; Sequence 3, Application US/09955225
; Publication No. US20030139588A9
GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09955225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-225-3
Alignment Scores:

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GenCore version 5.1.6  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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ALIGNMENTS

RESULT 1

US-09-995-225-3  
; Sequence 3, Application US/09995225  
; Publication No. US20020193584A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi Liang  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Pride, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: ASEN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253,404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255,366  
; PRIOR FILING DATE: 2000-12-12

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2	1592	100.0	918	10	US-09-995-225-3	Sequence 3, Appli
3	1592	100.0	918	13	US-10-297-908A-2	Sequence 2, Appli
4	1592	100.0	918	13	US-10-055-106C-1	Sequence 1, Appli
5	1592	100.0	918	15	US-10-188-405-9	Sequence 9, Appli
6	1592	100.0	1040	15	US-10-293-171-1	Sequence 1, Appli
7	1592	100.0	1318	15	US-10-017-161-1193	Sequence 1193, Ap
8	1592	100.0	2525	10	US-09-782-974C-81	Sequence 81, Appl
9	1592	100.0	113306	16	US-10-292-798-1007	Sequence 1007, Ap
10	1587	99.7	939	15	US-10-085-233B-3	Sequence 3, Appli
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12	1141	71.7	810	15	US-10-366-504-1	Sequence 21, Appl
13	674	42.3	447	10	US-09-782-974C-21	Sequence 20, Appl
14	250	15.7	1014	15	US-10-290-078-20	Sequence 7, Appli
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16	250	15.7	1358	15	US-10-167-192-4	Sequence 19, Appl
17	250	15.7	1359	15	US-10-290-078-19	Sequence 546, App
18	247	14.5	1014	15	US-10-225-567A-546	Sequence 9, Appli
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20	231.5	14.5	1146	15	US-10-225-567A-413	Sequence 417, App
21	231.5	14.5	1402	15	US-10-295-027-363	Sequence 363, App
22	231.5	14.5	1402	16	US-10-295-027-1038	Sequence 1038, Ap
23	231.5	14.5	1480	15	US-10-101-510-38	Sequence 38, Appl
24	231.5	14.5	1481	14	US-10-071-766-136	Sequence 136, App
25	231.5	14.5	1481	15	US-10-101-510-627	Sequence 627, App
26	231.5	14.5	1481	15	US-10-101-510-633	Sequence 633, App
27	231.5	14.5	1489	10	US-09-741-783-2	Sequence 2, Appli
28	231.5	14.5	1489	13	US-10-165-844-2	Sequence 881, App
29	231.5	14.5	1966	13	US-10-276-774-881	Sequence 21, Appl
30	231.5	14.5	1444	9	US-09-919-172-21	Sequence 85, Appl
31	231	14.5	1444	9	US-09-974-298-85	Sequence 2, Appli
32	231	14.5	1444	15	US-10-121-101B-2	Sequence 87, Appl
33	231	14.5	1041	15	US-10-321-807-87	Sequence 1, Appli
34	228	14.3	1041	9	US-09-826-791-1	Sequence 54, Appl
35	225	14.1	1026	10	US-09-991-225-54	Sequence 54, Appl
36	225	14.1	1026	13	US-10-369-405-54	Sequence 5, Appli
37	225	14.1	1039	17	US-10-182-605-1	Sequence 6, Appli
38	225	14.1	1041	9	US-09-826-791-5	Sequence 1, Appli
39	225	14.1	1041	9	US-09-866-230-6	Sequence 29, Appl
40	225	14.1	1041	10	US-09-828-478-1	Sequence 57, Appl
41	225	14.1	1041	10	US-09-991-225-29	Sequence 29, Appl
42	225	14.1	1041	13	US-10-343-650A-57	Sequence 29, Appl
43	225	14.1	1041	13	US-10-369-405-29	Sequence 1, Appli
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 Job time : 462 secs

; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: 60/253,404  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/255,366  
 ; PRIOR FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/270,286  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/282,365  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/270,266  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/282,032  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/282,358  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/282,356  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/290,917  
 ; PRIOR FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: 60/309,208  
 ; PRIOR FILING DATE: 2001-07-31  
 ; NUMBER OF SEQ ID NOS: 67  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 29  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: No. US20020193584A1 Sequence  
 US-09-995-225-26

Query Match 3.2%; Score 29; DB 9; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14  
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 ; Sequence 26, Application US/09995225  
 ; Publication No. US20030139588A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Ruoping  
 ; APPLICANT: Chu, Zhi Liang  
 ; APPLICANT: Dang, Huong T.  
 ; APPLICANT: Lowitz, Kevin P.  
 ; APPLICANT: Pride, Cameron  
 ; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G  
 ; FILE REFERENCE: AREN-0308  
 ; CURRENT FILING DATE: 2001-11-26  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: 60/170,496  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23938  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: 60/253,404  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/255,366  
 ; PRIOR FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/270,286  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/282,365  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/270,266  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/282,032  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/282,358  
 ; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282,356  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/290,917  
 ; PRIOR FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: 60/309,208  
 ; PRIOR FILING DATE: 2001-07-31  
 ; NUMBER OF SEQ ID NOS: 67  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 26  
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 ; ORGANISM: Artificial Sequence  
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 ; OTHER INFORMATION: No. US20030139588A9el Sequence  
 US-09-995-225-26

Query Match 3.2%; Score 29; DB 10; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
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RESULT 15  
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 ; Publication No. US20020193584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Ruoping  
 ; APPLICANT: Chu, Zhi Liang  
 ; APPLICANT: Dang, Huong T.  
 ; APPLICANT: Lowitz, Kevin P.  
 ; APPLICANT: Pride, Cameron  
 ; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
 ; FILE REFERENCE: AREN-0308  
 ; CURRENT FILING DATE: 2001-11-26  
 ; PRIOR FILING DATE: 2001-11-26  
 ; PRIOR APPLICATION NUMBER: 60/170,496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23938  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: 60/253,404  
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 ; PRIOR APPLICATION NUMBER: 60/255,366  
 ; PRIOR FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/270,286  
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 ; PRIOR APPLICATION NUMBER: 60/282,365  
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 ; PRIOR APPLICATION NUMBER: 60/270,266  
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 ; PRIOR APPLICATION NUMBER: 60/282,032  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/282,358  
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 ; PRIOR FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: 60/309,208  
 ; PRIOR FILING DATE: 2001-07-31  
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 ; SEQ ID NO 25  
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 ; OTHER INFORMATION: No. US20020193584A1el Sequence  
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Db 865 CTCCTCTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 924  
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Db 925 TGTGTTTGTGCGGT 939

RESULT 12  
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; Sequence 21, Application US/09782974C  
; Publication No. US20030082341  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: No. US20030082341a1 G Protein Coupled Receptor  
; FILE REFERENCE: 41USPRM311  
; CURRENT APPLICATION NUMBER: US/09/782,974C  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 09/714,449

; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/185,554  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/186,530  
; PRIOR FILING DATE: 2000-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 21  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-782-974C-21  
  
Query Match 33.3%; Score 306; DB 10; Length 447;  
Best Local Similarity 100.0%; Pred. No. 8.5e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60  
Db 402 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 343  
Qy 61 ATGAGCCTCTACTCATAGTGTCTTATGCGGCTGTGGTGTCTATTCATCTTTTC 120  
Db 342 ATGAGCCTCTACTCATAGTGTCTTATGCGGCTGTGGTGTCTATTCATCTTTTC 283  
Qy 121 CTCCTGTTGAAATGAACACCCGTCAGTGACCAACCATGGCGTCAATTAACCTTGGTGGT 180  
Db 282 CTCCTGTTGAAATGAACACCCGTCAGTGACCAACCATGGCGTCAATTAACCTTGGTGGT 223  
Qy 181 GTCACAGCCTTTCTGCTGACAGTGCATTCGCTTGACCTACCTCATCAAGAGACT 240  
Db 222 GTCACAGCCTTTCTGCTGACAGTGCATTCGCTTGACCTACCTCATCAAGAGACT 163  
Qy 241 TGGATGTTGGCTGCCCTCTCGAAATTTGTGAGTGCATCGCTGCACATCCACATGTAC 300  
Db 162 TGGATGTTGGCTGCCCTCTCGAAATTTGTGAGTGCATCGCTGCACATCCACATGTAC 103  
Qy 301 CTCACG 306  
Db 102 CTCACG 97

RESULT 13  
US-09-995-225-26/c  
; Sequence 26, Application US/09995225  
; Publication No. US20020193584A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi Liang  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Priddy, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
; FILE REFERENCE: AEN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938

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Db 12260 TACCAGTTCTTTAGGATCTATTACTGAATGTTGTGACGCAATCCCAATGCCGTGTAAACAGC 12319
Qy 781 AAGTTTCGCAATTTTATAACGAAATCTCTTGAGTGTAAACAGCAATTAAGCTGCTATGATTTG 840
Db 12320 AAGTTTCGCAATTTTATAACGAAATCTCTTGAGTGTAAACAGCAATTAAGCTGCTATGATTTG 12379
Qy 841 CTCTCTCTTCTCTTCTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT 900
Db 12380 CTCTCTCTTCTCTTCTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT 12439
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 12440 TGTGTTTTGTGCCGTTAG 12457

RESULT 10
US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCE: MPI2001-021PIRCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Query Match 94.4%; Score 867; DB 15; Length 1684;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 171 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 230
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTCTATTTCCATTTCTTTC 120
Db 231 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTCTATTTCCATTTCTTTC 290
Qy 121 CTCTGTGTGAAATGAACACCCGGTCAAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 180
Db 291 CTCTGTGTGAAATGAACACCCGGTCAAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 350
Qy 181 GTCCACAGCGTTTCTCTGTGACAGTCCATTTGGCTTGACCTACCTCATCAAGAAAGACT 240
Db 351 GTCCACAGCGTTTCTCTGTGACAGTCCATTTGGCTTGACCTACCTCATCAAGAAAGACT 410
Qy 241 TGGATGTTTGGGTGCCCTCTCTGCAAAATTTGTGAGTGCCATGTGACATCCACATGTAC 300
Db 411 TGGATGTTTGGGTGCCCTCTCTGCAAAATTTGTGAGTGCCATGTGACATCCACATGTAC 470
Qy 301 CTCAGTTTCTATCTATGTTGGTATCCTGTCACAGATACCTCATCTTCTTCTCAAGTGC 360
Db 471 CTCAGTTTCTATCTATGTTGGTATCCTGTCACAGATACCTCATCTTCTTCTCAAGTGC 530
Qy 361 AAAGACAAAGTGAATTTCTACAGAAAATCTGTCATGCTGTGGCTGCCAGTGTGTCATGTGG 420
Db 531 AAAGACAAAGTGAATTTCTACAGAAAATCTGTCATGCTGTGGCTGCCAGTGTGTCATGTGG 590
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Qy 421 ACGTGGTGTGATGTTCATTTGGTACCCTCGTGTCTCTCCGGTATGGAATCCCATGAGAA 480
Db 591 ACGTGGTGTGATGTTCATTTGGTACCCTCGTGTCTCTCCGGTATGGAATCCCATGAGAA 650
Qy 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCCTTACACATATGTGAAAATC 540
Db 651 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCCTTACACATATGTGAAAATC 710
Qy 541 ATCAACTATATGATGATGATCATTTTGTCTATAGCCGTTGCTGTGATCTCTGTGGTCTTCAG 600
Db 711 ATCAACTATATGATGATGATCATTTTGTCTATAGCCGTTGCTGTGATCTCTGTGGTCTTCAG 770
Qy 601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTTTTACTATCCACCCAGAG 660
Db 771 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTTTTACTATCCACCCAGAG 830
Qy 661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTGTCCTTGTGTTGTTCTTCTCCC 720
Db 831 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTGTCCTTGTGTTGTTCTTCTCCC 890
Qy 721 TACCAGTTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 780
Db 891 TACCAGTTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAGCAGC 950
Qy 781 AAGTTTGCATTTTATACGAATCTCTCTGAGTGTAAACAGCAATAGCTGCTATGATTTG 840
Db 951 AAGTTTGCATTTTATACGAATCTCTCTGAGTGTAAACAGCAATAGCTGCTATGATTTG 1010
Qy 841 CTCTCTTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 1011 CTCTCTTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1070
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 1071 TGTGTTTTGTGCCGTTAG 1088

RESULT 11
US-10-085-233B-3
; Sequence 3, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCE: MPI2001-021PIRCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(939)
US-10-085-233B-3

Query Match 94.1%; Score 864; DB 15; Length 939;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 25 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 84
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTGATTCATTTCTTCTTTC 120
Db 85 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTGATTCATTTCTTCTTTC 144
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Db 267 TGGATGTTGGGCTGCCCTTCGAAATTTGTAGTGCATGCTGCACATCCACATGTAC 326
Qy 301 CTCAGTTCCTATTCTATGTGTGATCCTCGGTGCACAGATACCTCATCTTCTTCAAGTGC 360
Db 327 CTCAGTTCCTATTCTATGTGTGATCCTCGGTGCACAGATACCTCATCTTCTTCAAGTGC 386
Qy 361 AAAGCAAAGTGGAAATCTTACAGAAAATGCGATGTGTGGTCCAGTCCAGTGGGATGTGG 420
Db 387 AAAGCAAAGTGGAAATCTTACAGAAAATGCGATGTGTGGTCCAGTGGGATGTGG 446
Qy 421 AGCGTGGTGAATGTCATGTGTGTACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 480
Db 447 AGCGTGGTGAATGTCATGTGTGTACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 506
Qy 481 TACAATGAGGACGACTGTTTAAATTTCAAAAGAGCTGTCTTACACATATGTGAAAATC 540
Db 507 TACAATGAGGACGACTGTTTAAATTTCAAAAGAGCTGTCTTACACATATGTGAAAATC 566
Qy 541 ATCAACTATATGATGATCAATTTTGTCTAGCCGTTGTGATCTGTGTCTTCCAG 600
Db 567 ATCAACTATATGATGATCAATTTTGTCTAGCCGTTGTGATCTGTGTCTTCCAG 626
Qy 601 GTCTTCATCATTTATGTGTGAGAGCTTACGCCACTCTTTACTATCCACAGGAG 660
Db 627 GTCTTCATCATTTATGTGTGAGAGCTTACGCCACTCTTTACTATCCACAGGAG 686
Qy 661 TTCTGGGCTCAGTGAAGAACCTATTTTATAGGGTCACTTGTGTGTCTTCC 720
Db 687 TTCTGGGCTCAGTGAAGAACCTATTTTATAGGGTCACTTGTGTGTCTTCC 746
Qy 721 TACCAGTCTTTAGGATCTATTACTTGAATGTGTGAGCGCAATCCAAATGCCCTGTAACAGC 780
Db 747 TACCAGTCTTTAGGATCTATTACTTGAATGTGTGAGCGCAATCCAAATGCCCTGTAACAGC 806
Qy 781 AAGGTGCAATTTTAAACGAATCTTCTTGAATGTGTGAGCGCAATCCAAATGCCCTGTAACAGC 840
Db 807 AAGGTGCAATTTTAAACGAATCTTCTTGAATGTGTGAGCGCAATCCAAATGCCCTGTAACAGC 866
Qy 841 CTCTCTTTGCTTTGGGGAGGACCAATGTTTAAAGCAAAAGATAAATTTGGCTTATGGAAT 900
Db 867 CTCTCTTTGCTTTGGGGAGGACCAATGTTTAAAGCAAAAGATAAATTTGGCTTATGGAAT 926
Qy 901 TGTGTTTGTGCCGTAG 918
Db 927 TGTGTTTGTGCCGTAG 944
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RESULT 9

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US-10-292-798-1007
; Sequence 1007, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABE, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: 2002-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1007
; LENGTH: 113306
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
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; FEATURE: (1)...(113306)
; LOCATION: (1)...(113306)
; NAME/KEY: CDS
; LOCATION: (201)...(207)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11526)...(12452)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37954)...(38097)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98732)...(98784)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112891)...(113106)
; US-10-292-798-1007

Query Match 100.0%; Score 918; DB 16; Length 113306;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Db 11540 ATGCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 11599
Qy 61 ATGAGCTCTTACTTCTATAGTCTTATTTGGGGGCTGTGGGTGTCTATTTCCATTTCTTTC 120
Db 11600 ATGAGCTCTTACTTCTATAGTCTTATTTGGGGGCTGTGGGTGTCTATTTCCATTTCTTTC 11659
Qy 121 CTCCTGGTGAATGAACACCCCGGTGAGTGACACCACTGCGGTGCTATTAACCTTGGTGGTG 180
Db 11660 CTCCTGGTGAATGAACACCCCGGTGAGTGACACCACTGCGGTGCTATTAACCTTGGTGGTG 11719
Qy 181 GTCCACAGCGTTTCTGCTGACAGTGCCTATTTGCTTGCCTTACCTCATCAAGAGACT 240
Db 11720 GTCCACAGCGTTTCTGCTGACAGTGCCTATTTGCTTGCCTTACCTCATCAAGAGACT 11779
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 11780 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 11839
Qy 301 CTCAGTTCCTATTCTATAGTGTGATCTCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 360
Db 11840 CTCAGTTCCTATTCTATAGTGTGATCTCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 11899
Qy 361 AAAGCAAAGTGGAAATCTTACAGAAAATGCGATGTGTGGTCCAGTGCATGTGG 420
Db 11900 AAAGCAAAGTGGAAATCTTACAGAAAATGCGATGTGTGGTCCAGTGCATGTGG 11959
Qy 421 AGCGTGGTGAATGTCATTTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Db 11960 AGCGTGGTGAATGTCATTTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 12019
Qy 481 TACAATGAGGACGACTGTTTAAATTTCAAAAGAGCTGTCTTACACATATGAAAATC 540
Db 12020 TACAATGAGGACGACTGTTTAAATTTCAAAAGAGCTGTCTTACACATATGAAAATC 12079
Qy 541 ATCAACTATATGATGATCAATTTTGTATAGCCGTTGCTGTGTGATCTGTGTGTCTTCCAG 600
Db 12080 ATCAACTATATGATGATCAATTTTGTATAGCCGTTGCTGTGTGATCTGTGTGTCTTCCAG 12139
Qy 601 GTCTTCATCATTTATGTGTGAGTGCAGAGCTACGCCACTTCTTACTATCCACAGGAG 660
Db 12140 GTCTTCATCATTTATGTGTGAGTGCAGAGCTACGCCACTTCTTACTATCCACAGGAG 12199
Qy 661 TTCTGGGCTCAGTGAAGAACCTATTTTATAGGGGCTCATCTTGTGTGTCTTCCCTCCC 720
Db 12200 TTCTGGGCTCAGTGAAGAACCTATTTTATAGGGGCTCATCTTGTGTGTCTTCCCTCCC 12259
Qy 721 TACCAGTCTTTAGGATCTATTACTTGAATGTGTGAGCGCAATCCAAATGCCCTGTAACAGC 780
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; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-055-106C-1

Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACATACCTCCAGGATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCCTGGCCACATACCTCCAGGATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTTCATAGTGCCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTTTC 120
DB 61 ATCAGCCTCTACTTTCATAGTGCCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTTTC 120

QY 121 CTCCTGTGAAATGAAACACCCGGTCTAGTACACACCCAGTCCGCTGCTTAACTTTGGTGG 180
DB 121 CTCCTGTGAAATGAAACACCCGGTCTAGTACACACCCAGTCCGCTGCTTAACTTTGGTGG 180

QY 181 GTCCACAGAGCTTTTCTGCTGACAGTGCCTTTCGCTTGGCTTACCTCATCAAGAAGACT 240
DB 181 GTCCACAGAGCTTTTCTGCTGACAGTGCCTTTCGCTTGGCTTACCTCATCAAGAAGACT 240

QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300
DB 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300

QY 301 CTCAGGCTTCTATTTCTATGTGTGTATCTCTGTCACACAGTACCTCATCTTCAAGTGC 360
DB 301 CTCAGGCTTCTATTTCTATGTGTGTATCTCTGTCACACAGTACCTCATCTTCAAGTGC 360

QY 361 AAAGACAAAGTGGAAATTTCTAGTGCCTTTCGCTTGGCTGCTGCTGCCAGTGTGGCATGTG 420
DB 361 AAAGACAAAGTGGAAATTTCTAGTGCCTTTCGCTTGGCTGCTGCTGCCAGTGTGGCATGTG 420

QY 421 ACGCTGTGTATGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
DB 421 ACGCTGTGTATGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480

QY 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 540
DB 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 540

QY 541 ATCAACTATATGATGATTTTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 600
DB 541 ATCAACTATATGATGATTTTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 600

QY 601 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 660
DB 601 GTCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 660

QY 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCTATCTTGTGTTGTTGTTGTTGTTGTT 720
DB 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCTATCTTGTGTTGTTGTTGTTGTTGTT 720
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RESULT 5

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US-10-188-405-9
; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Zhai, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1:el Receptors
; FILE REFERENCE: 018781-00841005
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR343
; US-10-188-405-9
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Query Match 100.0%; Score 918; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACATACCTCCAGGATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCCTGGCCACATACCTCCAGGATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTTCATAGTGCCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTTTC 120
DB 61 ATCAGCCTCTACTTTCATAGTGCCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTTTC 120

QY 121 CTCCTGTGAAATGAAACACCCGGTCTAGTACACACCCAGTCCGCTGCTTAACTTTGGTGG 180
DB 121 CTCCTGTGAAATGAAACACCCGGTCTAGTACACACCCAGTCCGCTGCTTAACTTTGGTGG 180

QY 181 GTCCACAGAGCTTTTCTGCTGACAGTGCCTTTCGCTTGGCTTACCTCATCAAGAAGACT 240
DB 181 GTCCACAGAGCTTTTCTGCTGACAGTGCCTTTCGCTTGGCTTACCTCATCAAGAAGACT 240

QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300
DB 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300

QY 301 CTCAGGCTTCTATTTCTATGTGTGTATCTCTGTCACACAGTACCTCATCTTCAAGTGC 360
DB 301 CTCAGGCTTCTATTTCTATGTGTGTATCTCTGTCACACAGTACCTCATCTTCAAGTGC 360

QY 361 AAAGACAAAGTGGAAATTTCTAGTGCCTTTCGCTTGGCTGCTGCTGCCAGTGTGGCATGTG 420
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241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300  
Db TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300  
301 CTCAGTTCCTTATCTATGTGTGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360  
Db CTCAGTTCCTTATCTATGTGTGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360  
361 AAAGCAAAAGTGAATCTTACAGAAAATCTGATGCTGTGGCTGCCAGTGTGGCATGTGG 420  
Db AAAGCAAAAGTGAATCTTACAGAAAATCTGATGCTGTGGCTGCCAGTGTGGCATGTGG 420  
421 AGCTGGTGAATGTCATGTGTGTGATCCCTGTGTGTCCTCCGGTATGGAATCCATGAGAA 480  
Db AGCTGGTGAATGTCATGTGTGTGATCCCTGTGTGTCCTCCGGTATGGAATCCATGAGAA 480  
481 TCAATGAGGAGCATGTTTAAATTTTCAAAAGAGCTTGTTCACATATGTGAAATC 540  
Db TCAATGAGGAGCATGTTTAAATTTTCAAAAGAGCTTGTTCACATATGTGAAATC 540  
541 ATCAACTATATGATAGTCAATTTTGTCTAGCCGTTGCTGTGATCTGTGTCCTCCAG 600  
Db ATCAACTATATGATAGTCAATTTTGTCTAGCCGTTGCTGTGATCTGTGTCCTCCAG 600  
601 GTCCTCATCATTTATGTTGATGTGAGAGCTACGCCACTTCTTACTATCCACAGAG 660  
Db GTCCTCATCATTTATGTTGATGTGAGAGCTACGCCACTTCTTACTATCCACAGAG 660  
661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCACTCTTGTGTGTTTCTTCC 720  
Db TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCACTCTTGTGTGTTTCTTCC 720  
721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTCCATCCATGCCCTGTAACAG 780  
Db TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTCCATCCATGCCCTGTAACAG 780  
781 AAGGTTGCAATTTTATAAGCAATCTTCTTGAAGTAAAGCAATGAGTCTATGATTTG 840  
Db AAGGTTGCAATTTTATAAGCAATCTTCTTGAAGTAAAGCAATGAGTCTATGATTTG 840  
841 CTTCTCTTTGCTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900  
Db CTTCTCTTTGCTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900  
901 TGTGTTTGTGCGCGTTAG 918  
Db TGTGTTTGTGCGCGTTAG 918

## RESULT 3

US-10-297-908A-2  
; Sequence 2, Application US/10297908A  
; Publication No. US20040029793A1  
; GENERAL INFORMATION:  
; APPLICANT: MORIYA, Takeo  
; APPLICANT: ITO, Takahashi  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: MIYAJIMA, No. US20040029793A1uyuki  
; TITLE OF INVENTION: No. US20040029793A1el G Protein-Coupled Receptor Protein and its  
; FILE REFERENCE: 2737 USOP  
; CURRENT APPLICATION NUMBER: US/10/297, 908A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/05061  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: JP 2000-184596  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: JP 2000-223887  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 2  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Human

US-10-297-908A-2  
Query Match 100.0%; Score 918; DB 13; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60  
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## RESULT 4

US-10-055-106C-1

;; PRIOR APPLICATION NUMBER: 60/309,208  
;; PRIOR FILING DATE: 2001-07-31  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 918  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-995-225-3

Query Match 100.0%; Score 918; DB 9; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCTGGCCACATACCTCCAGGAATTCCTTGGATCCTATAGTGACACCCCACTTA 60

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RESULT 2

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; Sequence 3, Application US/09995225  
; Publication No. US20030139588A9  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi-Liang  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Lowitz, Kevin P.  
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human C  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253,404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255,366  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/270,286  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,365  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/270,266  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,032  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,358  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,356  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/290,917  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/309,208  
; PRIOR FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 918  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-995-225-3

Query Match 100.0%; Score 918; DB 10; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	918	100.0	918	13	US-10-055-106C-1
5	918	100.0	918	15	US-10-188-405-9
6	918	100.0	1040	15	US-10-293-171-1
7	918	100.0	1318	15	US-10-017-161-1193
8	918	100.0	2525	10	US-09-782-974C-81
9	918	100.0	113306	16	US-10-232-798-1007
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c 18	26	2.8	26	9	US-09-995-225-54	Sequence 54, Appl
c 19	26	2.8	26	10	US-09-995-225-54	Sequence 54, Appl
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c 40	22	2.4	22	15	US-10-293-171-6	Sequence 6, Appl
c 41	21	2.3	21	13	US-10-297-908A-5	Sequence 5, Appl
c 42	21	2.3	21	15	US-10-293-171-3	Sequence 3, Appl
c 43	21	2.3	21	15	US-10-293-171-4	Sequence 4, Appl
c 44	21	2.3	21	15	US-10-293-171-8	Sequence 8, Appl
c 45	21	2.3	21	15	US-10-293-171-9	Sequence 9, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-995-225-3  
; Publication 3, Application US/0995225  
; Sequence No. US20020193584A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi Liang  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Pride, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253,404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255,366  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/270,286  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,365  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/270,266  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,032  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,358  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,356  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/290,917  
; PRIOR FILING DATE: 2001-05-14

ACCESSION AX451925  
 VERSION AX451925.1 GI:21698748  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Baughn, M.R., Graul, R.C., Walia, N.K., Gandhi, A.R., Hafalia, A.J.,  
 Rankumar, J., Tribouley, C.M., Thornton, M., Rallick, D.A., Yao, M.G.,  
 Elliott, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,  
 Roopa, R., Nguyen, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and  
 Policky, J.L.  
 TITLE G-protein coupled receptors  
 JOURNAL Patent: WO 0226825-A 22 04-APR-2002;  
 Incyte Genomics, Inc. (US)  
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 Location/Qualifiers  
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 Best Local Similarity 99.9%; Pred. No. 1.5e-219;  
 Matches 906; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
Deleersnijder W., Blockx, H. and de Moor, L.  
Human g-protein coupled receptor and uses thereof  
Patent: WO 0244212-A 1 06-JUN-2002;  
SOLVAY PHARMACEUTICALS B V (NL)  
FEATURES  
Location/Qualifiers  
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CDS

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Best Local Similarity 99.9%; Pred. No. 4.6e-225;  
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## RESULT 12

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LOCUS AC083865 218186 bp DNA linear PRI 26-JAN-2001
DEFINITION Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION AC083865
VERSION AC083865.2 GI:12545315
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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1 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Large-scale Mapping and Sequencing of Human Chromosome 7
Unpublished
2 (bases 1 to 218186)
Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
Direct Submission
Submitted (04-OCT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Direct Submission
Submitted (28-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgc@gsu.washington.edu
----- Project Information
Center project name: HsaChr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217693 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-fp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': mapping in progress
3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
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SeqDerMap FngRPrnt SeqDerMap FngRPrnt SeqDerMap FngRPrnt
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QY 901 TGTGTTTGTGCGGTAG 918

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AX521885 2525 bp DNA linear PAT 24-OCT-2002

LOCUS Sequence 81 from Patent WO02064789.

DEFINITION AX521885

ACCESSION AX521885

VERSION AX521885.1 GI:24410791

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Lind, P., Parodi, L.A., Vogeli, G. and Wood, L.S.

TITLE G protein-coupled receptor

JOURNAL Patent: WO 02064789-A 81 22-AUG-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 2525;

Best Local Similarity 100.0%; Pred. No. 1.9e-225;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ATCAGGCTCTACTTCTATAGTGTCTTATGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 120

Db 87 ATCAGGCTCTACTTCTATAGTGTCTTATGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 146

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Db 267 TGGATGTTGGGTGCGCTTCTGCAATTTGTGAGTGCCCATGTCGACATCCACATGTAC 326

QY 301 CTCACGTTCCTATCTATGTTGGTGGTCCCTGCTGACAGTGCCTATCTTCTTCAAGTGC 360

Db 327 CTCACGTTCCTATCTATGTTGGTGGTCCCTGCTGACAGTGCCTATCTTCTTCAAGTGC 386

QY 361 AAAGACAAAGTGAATCTTACAGAAATCTCATGCTGTGCTGCCAGTGTGTCATGTGG 420

Db 387 AAAGACAAAGTGAATCTTACAGAAATCTCATGCTGTGCTGCCAGTGTGTCATGTGG 446

QY 421 ACCTGTGTGATGTCATGTTGGTGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGA 480

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Db 927 TGTGTTTGTGCGGTAG 944

RESULT 11

AX646815 113306 bp DNA linear PAT 04-MAR-2003

LOCUS Sequence 1007 from Patent EP1270724.

DEFINITION AX646815

ACCESSION AX646815.1 GI:28799225

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.

TITLE Guanosine triphosphate-binding protein coupled receptors

JOURNAL Patent: EP 1270724-A 1007 02-JAN-2003;

National Institute of Advanced Industrial Science and Technology

(JP); Center for Advanced Science and Technology Incubation, Ltd.

(JP)

FEATURES

Location/Qualifiers

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LSVTAISQDILLFVFGGSHWFKQIIGLWNCVLCRNSPGLTFCFSQLSLFLHPAM

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ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 113306;

Best Local Similarity 100.0%; Pred. No. 2.9e-225;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 CTCCTGGTGAATAAGAACACCCGGTCACTGACACCATGGCGGTCTATTAACCTGGTGTG 180  
Db 463 CTCCTGGTGAATAAGAACACCCGGTCACTGACACCATGGCGGTCTATTAACCTGGTGTG 522  
Qy 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGCTTGACCTACCTCATCAAGAAGACT 240  
Db 523 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGCTTGACCTACCTCATCAAGAAGACT 582  
Qy 241 TGGATGTTTGGCTGCCCTCTTGAAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 300  
Db 583 TGGATGTTTGGCTGCCCTCTTGAAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 642  
Qy 301 CTCAGCTTCTTATCTATGTGTGTATCTCTGGTTCACAGATACCTCATCTTCTCAAGTGC 360  
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Db 1243 TGTGTTTGTGCGGTAG 1260

RESULT 9  
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LOCUS AX147836 2525 bp DNA linear PAT 08-JUN-2001  
DEFINITION Sequence 81 from Patent WO0136473.  
ACCESSION AX147836  
VERSION AX147836.1 GI:14346839  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,  
Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V.,

Sejltiz, T. and Huff, R.M.  
Novel g protein-coupled receptors  
Patent: WO 0136473-A 81 25-MAY-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.9e-225;  
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Db 87 ATCAGCCTCTACTTCTATGCTTATTTGGCGGCTGGTGGTGTCAATTTCCATCTTTTC 146  
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DEFINITION Sequence 53 from Patent WO02063004.  
ACCESSION AX709194  
VERSION AX709194.1 GI:29564788  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,  
Hafalia, A.J., Runkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.,  
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
Harland, L.  
TITLE G-protein coupled receptors  
JOURNAL Patent: WO 02063004-A 53 15-AUG-2002;  
Incyte Genomics, Inc. (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 1.8e-225;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS AX709195 1460 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 54 from Patent WO02063004.  
ACCESSION AX709195  
VERSION AX709195.1 GI:29564789  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,  
Hafalia, A.J., Runkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.,  
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
Harland, L.  
TITLE G-protein coupled receptors  
JOURNAL Patent: WO 02063004-A 54 15-AUG-2002;  
Incyte Genomics, Inc. (US)  
FEATURES  
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LOCUS Sequence 52 from Patent WO02063004.  
DEFINITION AX709193  
ACCESSION AX709193  
VERSION AX709193.1 GI:29564787  
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SOURCE Homo sapiens (human)  
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1  
Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,  
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,

Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.  
G-protein coupled receptors  
Patent: WO 02063004-A 52 15-AUG-2002;  
Incyte Genomics, Inc. (US)  
FEATURES  
Location/Qualifiers  
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Novel Polypeptide  
 Patent: JP 2003024082-A 1 28-JAN-2003;  
 Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)  
 OS Homo sapiens  
 PN JP 2003024082-A/1  
 PD 28-JAN-2003  
 PF 17-JAN-2002 JP 2002008881  
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 ACCESSION AY288420  
 VERSION AY288420.1 GI:32165523  
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 ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 918)  
 AUTHORS Fredriksson, R., Hoglund, P.J., Gloriam, D.E., Lagerstrom, M.C. and Schioth, H.B.  
 TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives  
 JOURNAL FEBS Lett. 554 (3), 381-388 (2003)  
 MEDLINE 22985413  
 PUBMED 14623098  
 REFERENCE 2 (bases 1 to 918)  
 AUTHORS Fredriksson, R., Hoglund, P.J., Gloriam, D.B.I., Lagerstrom, M.C. and Schioth, H.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala University, Box 593, Uppsala 75124, Sweden  
 FEATURES  
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 Best Local Similarity 100.0%; Pred. No. 1.7e-225; Indels 0; Gaps 0;  
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FEATURES		Pfizer Limited (GB) ; PFIZER INC. (US)	
source	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
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Query Match	100.0%; Score 918; DB 6; Length 918;		
Best Local Similarity	100.0%; Pred. No. 1.7e-225;		
Matches 918; Conservative	0; Mismatches 0; Indels 0; Gaps 0		
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Dd	1	ATGCTGTGGCCAAATACCTCCAGGAATTCCTCTCGATCCCTATAGTGACACCCACCTTA	60
Qy	61	ATCAGCCTCTACTTCATAGTGCTTATTGCGCGGCTGGTGGGTGCATTTCCTTCCTTTTC	120
Dd	61	ATCAGCCTCTACTTCATAGTGCTTATTGCGCGGCTGGTGGGTGCATTTCCTTCCTTTTC	120
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Dd	121	CTCTGGTGAATAAGAACACCGGTTCAGTGACCACCATGGCGGTCAATTAACCTGGTGG	180
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Dd	181	GTCCACACAGGTTTTCTGTGCAGCTGCCATTTCGCTTGACCTACTCATCAAGAAGACT	240
Qy	241	TGGATGTTTGGCTGCCCTCTCTGCAAAATTGTGAGTGCCATGCTGCACATCCACATGTAC	300
Dd	241	TGGATGTTTGGCTGCCCTCTCTGCAAAATTGTGAGTGCCATGCTGCACATCCACATGTAC	300
Qy	301	CTCAGTTTCCTATTCTATGTGGTGATCTCTGGTCCACAGATACCTCATCTTCCTCAAGTGC	360
Dd	301	CTCAGTTTCCTATTCTATGTGGTGATCTCTGGTCCACAGATACCTCATCTTCCTCAAGTGC	360
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Dd	361	AAAGCAAAGTGGAAATCTACAGAAAATGTGCATGTGTGGCTGCAGTCTGGCATGTGG	420
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Dd	421	ACGCTGGTGATTGTCAATTGTGGTACCCCTGGTGTCTCCGGTATGGAAATCCATCAGGAA	480
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Dd	601	GTCTTTCATCTATTGTTGATGGTGAGAGCTACGCCACTCTTTACTATCCACCAGAG	660
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Dd	661	TTCTGGGCTCAGCTGAAAAAACCCTATTTTTTATAGGGGTCACTCTGTGTTTCTCTGCC	720
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Dd	721	TACAGTTCTTTTAGATCTATTACTTGAAATGTTGTGACGCTTCCAAATGCCCTGTAAACAG	780
Qy	781	AAGGTTGCATTTTATAACGAAATCTCTTTAGTGTAAACAGCAATTAGCTGCTATGATTG	840
Dd	781	AAGGTTGCATTTTATAACGAAATCTCTTTAGTGTAAACAGCAATTAGCTGCTATGATTG	840
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Db		901	TGCTTTTGCCGTAG	918
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LOCUS			918 bp	DNA linear PAT 26-SEP-2002
DEFINITION			Sequence 3 from Patent WO0242461.	
ACCESSION			AX498180	
VERSION			AX498180.1	GI:23343111
KEYWORDS			Homo sapiens (human)	
SOURCE			Homo sapiens	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE			1	
JOURNAL			Chen,R., Chu,Z.L., Dang,H.T., Lowitz,K.P. and Pride,C.	
FEATURES			Endogenous and non-endogenous versions of human g protein-coupled receptors	
source			Patent: WO 0242461-A 3 30-MAY-2002;	
			Arena Pharmaceuticals, Inc. (US)	
			Location/Qualifiers	
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			/organism="Homo sapiens"	
			/mol_type="unassigned DNA"	
			/db_xref="taxon:9606"	
ORIGIN				
Query Match			100.0%; Score 918; DB 6; Length 918;	
Best Local Similarity			100.0%; Pred. No. 1.7e-225;	
Matches 918; Conservative			0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTAGCACCCCACCTTA	60	
Db	1	ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTAGCACCCCACCTTA	60	
Qy	61	ATACGCCCTACTTCATAGTGTCTTATTGGCGGGCTGGTGGTGCATTTCCATTCTTTTC	120	
Db	61	ATACGCCCTACTTCATAGTGTCTTATTGGCGGGCTGGTGGTGTGCATTTCCATTCTTTTC	120	
Qy	121	CTCCTGTGGTAAATGAACACCCGCTCAGTCACCACCATGGCGGTCACTTAACCTGGTGGT	180	
Db	121	CTCCTGTGTAAATGAACACCCGCTCAGTCACCACCATGGCGGTCACTTAACCTGGTGGT	180	
Qy	181	GTCACAGCGTTTTTCTGTGACAGTGCCATTTGCTGTGACCTACCTCATCAAGAAGACT	240	
Db	181	GTCACAGCGTTTTTCTGTGACAGTGCCATTTGCTGTGACCTACCTCATCAAGAAGACT	240	
Qy	241	TGGATGTTTGGGTCGCCCTTCTGCAATTTGTGAGTGCCATGTGCACATCCACATGTAC	300	
Db	241	TGGATGTTTGGGTCGCCCTTCTGCAATTTGTGAGTGCCATGTGCACATCCACATGTAC	300	
Qy	301	CTCACGPTTCCTATTCATGTGGTGATCCTCGTCCAGCATACCTCATCTTTCAAGTGC	360	
Db	301	CTCACGPTTCCTATTCATGTGGTGATCCTCGTCCAGCATACCTCATCTTTCAAGTGC	360	
Qy	361	AAAGACAAAGTGGMAATCTACAGAAAACCTCATGCTGTGGCTGCCAGTGTGGCATGTGG	420	
Db	361	AAAGACAAAGTGGMAATCTACAGAAAACCTCATGCTGTGGCTGCCAGTGTGGCATGTGG	420	
Qy	421	ACGCTGGTGATTGTCACTTGTGGTACCCCTCGTTGTCTCCCGGTATGGAATCCATGAGAA	480	
Db	421	ACGCTGGTGATTGTCACTTGTGGTACCCCTCGTTGTCTCCCGGTATGGAATCCATGAGAA	480	
Qy	481	TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTCCTTACACATATGTGAAAAATC	540	
Db	481	TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTCCTTACACATATGTGAAAAATC	540	
Qy	541	ATCAACTATATGATAGTCACTTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTCCAG	600	
Db	541	ATCAACTATATGATAGTCACTTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTCCAG	600	
Qy	601	GTCTTCATATTATGTTGATGGTGCAGAACTACGCCACTCTTTTACTATATCCACAGGAG	660	



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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 12:45:39 ; Search time 3929 Seconds  
(without alignments)  
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Perfect score: 918

Sequence: 1 atgcctggccacaataacctc.....attgtgtttgtgcgcttag 918

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_htg.\*

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5: gb\_ov.\*

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7: gb\_ph.\*

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9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_on.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

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27: em\_sts.\*

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29: em\_vi.\*

30: em\_htg\_hum.\*

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32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

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37: em\_htg\_vrt.\*

38: em\_sy.\*

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40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	918	100.0	918	6	AX481576	Sequence
2	918	100.0	918	6	AX498180	Sequence
3	918	100.0	918	6	BD105324	Novel G p
4	918	100.0	918	6	BD187510	Novel Pol
5	918	100.0	918	9	AY288420	Homo sapi
6	918	100.0	1336	6	AX709193	Sequence
7	918	100.0	1340	6	AX709194	Sequence
8	918	100.0	1460	6	AX709195	Sequence
9	918	100.0	2525	6	AX147836	Sequence
10	918	100.0	2525	6	AX521885	Sequence
11	918	100.0	113306	6	AX646815	Sequence
12	918	100.0	218186	9	AC083865	Homo sapi
13	916.4	99.8	1051	6	AX453412	Sequence
14	913.2	99.5	164055	2	AC146385	Sequence
15	895	97.5	1499	6	AX451925	Sequence
16	690	75.2	972	6	AX657538	Sequence
17	636.4	69.3	918	10	AY288427	Mus muscu
18	636.4	69.3	206999	10	AC122886	Mus muscu
19	634.8	69.2	167316	2	AC078995	Mus muscu
20	525	57.2	228766	2	AC099132	Rattus no
21	456	49.7	456	9	AY255538	Homo sapi
22	437.2	47.6	140539	2	AC079758	Homo sapi
23	433	47.2	744	10	AY288432	Rattus no
24	390	42.5	447	6	AX147776	Sequence
25	390	42.5	447	6	AX521825	Sequence
26	276.8	30.2	393	10	AY255553	Mus muscu
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29	144.8	15.8	897	6	BD182016	Novel G p
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31	105	11.4	225912	2	AC084210	Homo sapi
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# ALIGNMENTS

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DEFINITION	AX481576				
ACCESSION	AX481576				
VERSION	AX481576.1	GI:22316490			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					

Pred. No. is the number of results predicted by chance to have a

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Db      |||
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QY      41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
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US-10-055-106C-2 (1-305) x AAL53413 (1-1684)

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 Qy 301 CysValLeuCysArg 305  
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RESULT 15

AAD37670

ID AAD37670 standard; cDNA; 1499 BP.

XX XX

AC AAD37670;

XX XX

DT 27-AUG-2002 (first entry)

XX Human G-protein coupled receptor-6 (GCRC-6) cDNA.

XX Human; G-protein coupled receptor-6; GCRC-6; atherosclerosis; cancer;  
 cell proliferative disorder; gastrointestinal; autoimmune; metabolic;  
 neurological; inflammatory; cardiovascular; viral infection; anorexia;  
 KW cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;  
 KW Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;  
 KW rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;  
 KW osteoporosis; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 381..1400

XX FT /tag= a

XX FT /product= "Human GCRC-6 protein"

XX WO200226825-A2.

XX 04-APR-2002.

XX 28-SEP-2001; 2001WO-US030661.

XX 29-SEP-2000; 2000US-0236546P.

XX 13-OCT-2000; 2000US-0240589P.

XX 20-OCT-2000; 2000US-0242232P.

XX 20-OCT-2000; 2000US-0242322P.

XX 03-NOV-2000; 2000US-0245855P.

XX 03-NOV-2000; 2000US-0245900P.

XX 19-NOV-2000; 2000US-0247587P.

XX 19-NOV-2000; 2000US-0249343P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn ME, Graul RC, Walia NK, Gandhi AR, Hafalia AJA;

XX Ramkumar J, Tribouley CM, Thornton M, Kallick DA, Yao MG;

XX Elliott VS, Burford N, Khan FA, Yue H, Lu Y, Arvizu C, Roopa R;

XX Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;

XX WPI; 2002-426012/45.

XX P-PSDB; AAE23414.

XX Novel G-protein coupled receptor polypeptides referred as GCRC peptides,  
 PT useful for treating multiple sclerosis, cholecystitis heart failure,  
 PT angina pectoris, rheumatoid arthritis, obesity, osteoporosis.

XX Claim 83; Page 140; 147pp; English.

XX The invention relates to human G-protein coupled receptor (GCRC 1-16)  
 CC polypeptides and polynucleotides. Sequences of the invention are useful  
 CC for the diagnosis, treatment and prevention of cell proliferative (e.g.  
 CC cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's  
 CC disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,  
 CC heart failure), gastrointestinal (e.g. anorexia, cholecystitis),  
 CC autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)  
 CC and metabolic disorders (e.g. obesity, osteoporosis), viral infections  
 CC atherosclerosis and hepatitis. GCRC proteins are useful for identifying  
 CC compounds that modulate, mimic and block olfactory and taste sensations.  
 CC They are also useful for identifying GCRC modulators. GCRC DNAs are  
 CC useful in gene therapy. The present sequence is human GCRC-6 cDNA

XX SQ Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.03e-124 Length: 1499

Score: 1547.00 Matches: 303

Percent Similarity: 99.34% Conservative: 0

Best Local Similarity: 99.34% Mismatches: 2

Query Match: 97.17% Indels: 2

DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x AAD37670 (1-1499)

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Db 325 CTCAGTTCCTATTCTATGCTGATCTCTGGTCCACAGATACCTCATCTTCTTCAAGTGC 384  
QY 121 LysAspLysValGluPheTyrArgLysLeuHsAlaValAlaAlaSerAlaGlyMetTrp 140  
Db 385 AAAGCAAAAGTGGAAATTCACAGAAATGCAATGCTGGCTGCCAGTGGCATGTGG 444  
QY 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHsGluGlu 160  
Db 445 AGCTGGTGGTTCATTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 504  
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Db 565 ATCACTATATGATGATGATTTTGTATAGCGGTGCTGCTGCTGCTGCTGCTGCTGCT 624  
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuValArgHsSerLeuLeuSerHsGlnGlu 220  
Db 625 GTCTTCATCATTTATGTTGATGCTGAGAGAGCTACGCCACTCTTTACTATCCACCAGAG 684  
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
Db 685 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCACTCTGTTGTTGTTCTTCC 744  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHsSerAsnAlaCysAsnSer 260  
Db 745 TACCAGTCTTTAGGATCTATTACTTGAATTTGTGACGCTTCCCAATGCCCTGTAGCAGC 804  
QY 261 LysValAlaPheTyrHsGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
Db 805 AAGTTGGCAATTTATACCAATCTTCTTGAGTGTACAGCAATAGCTGCTATGATTG 864  
QY 281 LeuLeuPheValPheGlyGlySerHsIleTyrPheLysGlnLysIleGlyLeuTrpAsn 300  
Db 865 CTCTCTCTGTTCTTTGGGGAGCCATCTGTTTACGAAAGATATTTGGCTTATGGAAT 924  
QY 301 CysValLeuCysArg 305  
Db 925 TGGTTTTTGGCGGT 939  
RESULT 14  
ID AAL53413 standard; cDNA; 1684 BP.  
AC AAL53413;  
XX AAL53413;  
XX 12-DEC-2002 (first entry)  
DT 1684 nt cDNA of human G-protein coupled receptor type protein.  
DE  
XX Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;  
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;  
XX antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;  
XX cardiant; dermatological; antiinfertility; hepatotropic; antiallergic;  
XX antipsoriatic; ophthalmological; antianginal; antithyroid; anticonvulsant;  
XX antirheumatic; antiarthritic; G-protein coupled receptor; family I;  
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;  
XX skeletal, bone metabolism disorder; bone marrow mononuclear disorder;  
XX cellular proliferative; differentiative disorder; hormonal disorder;  
XX neurological disorder; cardiovascular disorder; viral disease; pain;  
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;  
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;  
XX viral meningitis; fungal meningencephalitis; multiple sclerosis;  
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;  
XX Huntington's disease; heart failure; angina pectoris; dermatitis;  
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;

inflammatory bowel disease; asthma; graft-versus-host disease; allergy;  
conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;  
transgenic animal; human; gene; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 147..1088  
/\*tag= a  
/product= "Human G-protein coupled receptor type protein  
93870"  
WO200270657-A2.  
12-SEP-2002.  
28-FEB-2002; 2002WO-US006455.  
01-MAR-2001; 2001US-0272677P.  
(MILL-) MILLENNIUM PHARM INC.  
Glucksmann WA;  
WPI; 2002-732793/79.  
P-PSDB; AAO22919.  
New G-protein coupled receptor used in receptor assays as a target for  
diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
inflammatory disorders, platelet disorders, skeletal or bone metabolism  
disorders.  
Claim 5; Page 99-100; 105pp; English.  
The invention relates to an isolated polypeptide, which is a G-protein  
coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
receptor type proteins (GPCRs), designated the 93870 receptor. The  
polypeptides, nucleic acid molecules and antibodies of the invention are  
useful in screening assays, predictive medicine (e.g. diagnostic assays,  
monitoring clinical trials or pharmacogenetics), or in methods of  
treating (e.g. therapeutic and prophylactic). They are useful in  
treating and diagnosing conditions related to aberrant activity or  
expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
inflammatory disorders, platelet disorders, skeletal or bone metabolism  
disorders, or bone marrow mononuclear disorders, as well as cellular  
proliferative and/or differentiative disorders, hormonal disorders, liver  
neurological disorders, cardiovascular disorders, viral diseases, liver  
disorders, and pain and metabolic disorders. Conditions that can be  
treated include cancer, diabetes mellitus, hypothyroidism,  
hyperthyroidism, reproductive or fertility disorders, multiple sclerosis,  
viral meningitis, fungal meningencephalitis, ataxia-telangiectasia,  
Alzheimer's disease, Parkinson's disease, angina pectoris, myocardial  
Huntington's disease, heart failure, angina pectoris, Crohn's disease,  
inflammation, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
transgenic animals are useful for studying the function and/or activity  
of a 93870 protein and for identifying and/or evaluating modulators of  
93870 activities. The polynucleotides of the invention can be used in  
gene therapy. This polynucleotide sequence represents the cDNA of the  
1684 nucleotide human G-protein coupled receptor type protein of the  
invention  
Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 4.03e-128 Length: 1684  
Score: 1587.00 Matches: 304  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.67% Mismatches: 0  
Query Match: 99.69% Indels: 0  
DB: 6 Gaps: 0

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Db 12080 ATCAACTATATGATGTCATTTTGTATAGCGGTGCTGATTCCTGTTGGTCTCCAG 12139
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 12140 GTCCTTCATCATATGTTGATGGTGAGAGCTAGCCCACTCTTTTACATATCCACGAGAG 12199
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 12200 TTCGGGCTAGCTGAAACCTATTTTATAGGGTCACTCTTTGTTGTTCTTCCC 12259
Qy 241 TyrGlnPhePheArgIleTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 12260 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGACGCAATCCCAATGCCGTGAACAGC 12319
Qy 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 12320 AAGTTGCAATTTATACGAATCTCTTGTAGTGACAGCAATAGCTGCTATGATTTG 12379
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db 12380 CTTCCTCTTTGCTTTGGGGAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 12439
Qy 301 CysValLeuCysArg 305
Db 12440 TGTGTTTGTGCCGT 12454

RESULT 13
AAL53414
ID AAL53414 standard; DNA; 939 BP.
XX AC AAL53414;
XX DE 12-DEC-2002 (first entry)
XX DE 939 nt coding DNA of a human G-protein coupled receptor type protein.
XX KW Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory;
KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
KW cardiac; dermatological; antinfertility; hepatotropic; antiallergic;
KW antipsoriatic; ophthalmological; antiangnal; antithyroid; anticonvulsant;
KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;
KW 93870 receptor; immune; inflammatory disorder; platelet disorder;
KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
KW cellular proliferative; differentiative disorder; hormonal disorder;
KW neurological disorder; cardiovascular disorder; viral disease; pain;
KW liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
KW viral meningitis; fungal meningoencephalitis; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
KW Huntington's disease; heart failure; angina pectoris; dermatitis;
KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
KW transgenic animal; human; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 1..939
XX FT /*tag= a
XX FT /partial
XX FT /product= "Human G-protein coupled receptor type protein
XX FT 93870"
XX FT /note= "No stop codon"
XX PN WO200270657-A2.
XX XX
XX PD 12-SEP-2002.
XX XX
XX PF 28-FEB-2002; 2002WO-US006455.
XX XX

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PR 01-MAR-2001; 2001US-0272677P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Glucksmann MA;
XX DR WPI; 2002-732793/79.
XX DR P-PSDB; AAO22919.
XX PT New G-protein coupled receptor used in receptor assays as a target for
XX PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
XX PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
XX PT disorders.
XX PS Claim 5; Page 101-103; 105pp; English.
XX CC The invention relates to an isolated polypeptide, which is a G-protein
XX CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
XX CC receptor type proteins (GPCRs), designated the 93870 receptor. The
XX CC polypeptides, nucleic acid molecules and antibodies of the invention are
XX CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
XX CC monitoring clinical trials or pharmacogenetics), or in methods of
XX CC treatment (e.g. therapeutic and prophylactic). They are useful in
XX CC treating and diagnosing conditions related to aberrant activity or
XX CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
XX CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
XX CC disorders, or bone marrow mononuclear disorders, as well as cellular
XX CC proliferative and/or differentiative disorders, hormonal disorders,
XX CC neurological disorders, cardiovascular disorders, viral diseases, liver
XX CC disorders, and pain and metabolic disorders. Conditions that can be
XX CC treated include cancer, diabetes mellitus, hypothyroidism,
XX CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
XX CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,
XX CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
XX CC Huntington's disease, heart failure, angina pectoris, myocardial
XX CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
XX CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
XX CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
XX CC transgenic animals are useful for studying the function and/or activity
XX CC of a 93870 protein and for identifying and/or evaluating modulators of
XX CC 93870 activities. The polynucleotides of the invention can be used in
XX CC gene therapy. This polynucleotide sequence represents the 939 nucleotide
XX CC DNA of the human G-protein coupled receptor type protein of the invention
XX SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,09e-128 Length: 939
Score: 1587.00 Matches: 304
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 99.69% Indels: 0
DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x AAL53414 (1-939)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 25 ATGCTGGCCACAAATACCTCCAGGAATTCCTTGGATCCTATAGTAGACACCCACTTA 84
Qy 21 IleSerLeuTyrPheIleValIleGlyGlyLeuValGlyValIleSerLeuPhe 40
Db 85 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGGTGTGGGTGTCATTTCCTTTTC 144
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal 60
Db 145 CTCCTGGTGAATGAACACCCGGTCAGTGACCACCATCGCGGTCAATTAACITGGTGG 204
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuLeuLysLysThr 80
Db 205 GTCCACAGCGGTTTTCTGCTGACGTGCCATTTCGCTTGACCTACCTCATCAAGAGACT 264
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100

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Db 207 GTCCACAGGTTTCTTCGTGACAGTGCCATTCGCTGACCTACCTCATCAAGAAGACT 266
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 267 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCATCCACATGATGAC 326
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 327 CTCAGGTTCCATTTCTATGTGTGTGATCTCTGGTCCACAGATACCTCATCTTCTCAAGTGC 386
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
Db 387 AAAGCAAAAGTGGAAATTTACAGAAACTGCATGCTGTGGCTGCCAGTCTGGCATGTGG 446
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 447 AGCTGGTGAATTTGATGTGTGTGATGACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 506
Qy 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 507 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTACACATATGTGAAAATC 566
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 567 ATCAACTATATGATAGTCAATTTTGTGATAGCGGTGCTGTGATCTGTGTCTTCCAG 626
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 627 GTCTTCATCATTTATGTTGATGTGTGAGAGCTACGCCACTCTTTACTATCCACCAGGAG 686
Qy 221 PheTyrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 687 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTGTGTGTCTTCTTCC 746
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 747 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGACGCAATTCCAATGCCCTGTAAACAG 806
Qy 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 807 AAGGTTGCATTTTATACGAAATCTTCTTGAGTGTAAACGCAATTAGCTGCTATGATTG 866
Qy 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTyrAsn 300
Db 867 CTTCCTTTGCTTTGGGGGAAGCCATTGTTTAAACAAAGATAATTGGCTTATGGAAT 926
Qy 301 CysValLeuCysArg 305
Db 927 TGTGTTTGTGCGGT 941

RESULT 12
ID ADC86554 standard; DNA; 113306 BP.
XX
AC ADC86554;
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE Human GPCR gene SEQ ID NO:1007.
XX
XX ds; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
XX Homo sapiens.
XX
XX BP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX
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XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX WPI; 2003-315783/31.
XX
XX P-PSDB; ADC86555.
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1007; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.67e-126 Length: 113306
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-055-106C-2 (1-305) x ADC86554 (1-113306)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 11540 ATGCTGGCCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTACACCCCACTTA 11599
Qy 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 11600 ATCAGCTCTACTTCAATAGTCTTATTTGGGGGCTGTGGGTGTCATTTCCATTCCTTTC 11659
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 11660 CTCCTGGTGAATGAACACCCGCTCAGTCACCATGGCGGTCAATTAACCTGGTGGTG 11719
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuIleLysLysThr 80
Db 11720 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 11779
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 11780 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGAC 11839
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleuIlePhePheLysCys 120
Db 11840 CTCACGTTCTTATTTCTATGTGGTATCTCTGTCACCAAGATACCTCATCTTCTTCAAGTGC 11899
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
Db 11900 AAAGCAAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCATGCTGGCATGCG 11959
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 11960 ACGCTGGTGAATTTGATTTGGTACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 12019
Qy 161 TyrAsnGluGluHisCysPheLysPheHisLysGlnLeuAlaTyrThrTyrValLysIle 180
Db 12020 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 12079
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
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Db      643  CTCACGTTCTTATCTATGCTGATCTCTGTCACACAGATACCTCATCTCTTCAAGTGC 702
Qy      121  LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db      703  AAAGACAAAGTGAATTCACAGAAACATGCGTGTGGCTGCCAGTGGCATGTGG 762
Qy      141  ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db      763  ACGTGTGATGTCATTGTGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 822
Qy      161  TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIleVal 180
Db      823  TACAATGAGAGACACTGTTTAAATTCACAAGAGCTTGTCTACACATATGTGAATC 882
Qy      181  IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
Db      883  ATCACTATATGATAGTCACTTTTGTGCATAGCGTGTGTGATCTGTGTCTTCAG 942
Qy      201  ValPheIleIleValMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db      943  GTCTTCATCATATTATGTGTGTGTGCGAAGAGCTACGCCCTCTTTACTATCCACAGGAG 1002
Qy      221  PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db      1003  TTCTGGCTCAGCTGAAACCACTATTTTATAGGGGTCTATCTCTGTTGTTCTCTCC 1062
Qy      241  TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnLysSer 260
Db      1063  TACCAGTCTTTAGGATCTATTACTTTGAATGTGTGACGATTCCTCAATCCCTGTACAGC 1122
Qy      261  LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db      1123  AAGTTGTCATTTTAAAGCAATCTCTTGAGTGTACAGCAATTAGCTGCTATGATTG 1182
Qy      281  LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db      1183  CTCTCTCTTCTCTTGGGGAGGCCATTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 1242
Qy      301  CysValLeuCysArg 305
Db      1243  TGTGTTTGTGGCGT 1257

RESULT 10
AAH51009
ID AAH51009 standard; DNA; 2525 BP.
XX AC AAH51009;
XX DT
XX DE
XX DX
XX KW G protein-coupled receptor; nPCR; seven transmembrane receptor;
XX KW signal transduction; schizophrenia; thyroid disorder; renal failure;
XX KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
XX KW cardiovascular disease; proliferative disorder; hormonal disorder;
XX KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
XX KW attention deficit-hyperactivity disorder/attention deficit disorder;
XX KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
XX KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
XX KW neuroprotective; ds.
XX OS Homo sapiens.
XX FN WO200136473-A2.
XX PD 25-MAY-2001.
XX PF 16-NOV-2000; 2000WO-US0311581.
XX PR 16-NOV-1999; 99US-0165838P.
XX PR 17-NOV-1999; 99US-0166071P.
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PR 19-NOV-1999; 99US-0166578P.
PR 28-DEC-1999; 99US-0173396P.
PR 22-FEB-2000; 2000US-0184129P.
PR 28-FEB-2000; 2000US-0185421P.
PR 28-FEB-2000; 2000US-0185554P.
PR 02-MAR-2000; 2000US-0186530P.
PR 03-MAR-2000; 2000US-0186811P.
PR 09-MAR-2000; 2000US-0188114P.
PR 17-MAR-2000; 2000US-0190310P.
PR 21-MAR-2000; 2000US-0190800P.
PR 20-APR-2000; 2000US-0198568P.
PR 02-MAY-2000; 2000US-0201190P.
PR 08-MAY-2000; 2000US-0203111P.
PR 25-MAY-2000; 2000US-0207094P.
XX (PFAA ) PHARMACIA & UPJOHN CO.
PA Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J,
XX Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
PI WPI; 2001-389826/41.
XX P-PSDB; AAG80969.
PT New G protein-coupled receptor (nPCR-x) and its encoding polynucleotide
XX useful for diagnosing and treating e.g. schizophrenia.
PS Claim 4; Page 89-90; 261pp; English.
XX The present invention relates to novel G protein-coupled receptors
CC (nPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC also known as seven transmembrane receptors and function in signal
CC transduction. The nPCRx coding sequences are useful for screening a
CC human to diagnose a disorder affecting the brain or a genetic
CC predisposition, specifically schizophrenia. nPCRx are useful for
CC identifying compounds useful for treating schizophrenia. Detection of
CC nPCRx in a sample is useful as a diagnostic tool for diseases or
CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular
CC diseases, proliferative disorders and hormonal disorders. Modulators of
CC nPCRx activity have the utility for treating neurological disorders,
CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
CC disorder/attention deficit disorder), and neuronal disorders such as
CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.
CC Additional disorders include inflammatory conditions (e.g. Crohn's
CC disease), rheumatoid arthritis, autoimmune disorders, cancers,
CC respiratory ailments such as asthma, and inflammatory diseases e.g.
XX inflammatory bowel disease
XX SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,34e-128 Length: 2525
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-055-106C-2 (1-305) x AAH51009 (1-2525)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 27 ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 86
Qy 21 IleSerLeuTyrPheIleValIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 87 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGGTGGTGGGTGTCATTTCCTTTTC 146
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 147 CTCCTGGTGAATGAACACCGGTGAGTGCACCACTGGGGGTGATTAATTTCCTGGTGTG 206
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Db 463 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGGAGTGCCATGTCACATGATGAC 522  
Qy 101 LeuThrPheLeuPheTyrValValLeuValThrArgTyrLeuLeuPhePheLeuValCys 120  
Db 523 CTCAGTTCCTATTCTATGTTGGTATCTCTGTCACAGATACCTCTCTTCAATGTC 582  
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLaserAlaGlyMetTyr 140  
Db 583 AAGACAAAGTGAATCTACAGAAACTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 642  
Qy 141 ThrLeuValIleValIleValIleValIleValIleValIleValIleValIleValIle 160  
Db 643 ACGCTGGGATGTGATGTGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702  
Qy 161 TyrAsnGluGluHisCysPhePhePheHisLysGluLeuAlaTyrThrTyrValIle 180  
Db 703 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTACATATGTGAAATC 762  
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
Db 763 ATCAACTATATGATAGTCATTTTGTGTATAGCCGTGCTGTGTGTGTGTGTGTGTGT 822  
Qy 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
Db 823 GTCTTCATCATATTGTTGATGTTGTCAGAGAGCTAGCCCACTCTTTACTATCCACAGAG 882  
Qy 221 PheTrpAlaGlnLeuLysLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
Db 883 TTCTGGGCTAGCTGAAACCTATTTTATAGGGGTCACTCTGTTGTTGTTGTTGTTGTT 942  
Qy 241 TyrGlnPhePheAspGlyTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
Db 943 TACAGTTCCTTAGAATCTATTCTGATGTTGTGAGCATTCATGCTGTTAAACAGC 1002  
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
Db 1003 AAGGTTGCATTTTATAACAAATCTCTCTGAGTGTAAACAGCAATAGCTGATGATTG 1062  
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
Db 1063 CTTCCTCTTGTCTTTGGGGAGGCCATGTTGTTTAAAGCAAAAGATAATGGCTTATGGAAT 1122  
Qy 301 CysValLeuCysArg 305  
Db 1123 TGTGTTTGTGCCGT 1137  
RESULT 9  
AAF88585  
ID AAF88585 standard; cDNA; 1460 BP.  
AC AAF88585;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Human GCREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.  
XX  
KW GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
KW cerebrotrophic; antinflammatory; virucide; antibacterial; fungicide;  
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200263004-A2.  
XX  
PD 15-AUG-2002.  
XX  
PF 06-FEB-2002; 2002WO-US003635.  
XX  
PR 07-FEB-2001; 2001US-0267322P.

PR 23-FEB-2001; 2001US-0271215P.  
PR 08-MAR-2001; 2001US-0274551P.  
PR 23-MAR-2001; 2001US-0278507P.  
PR 30-MAR-2001; 2001US-0280597P.  
PR 02-APR-2001; 2001US-0281107P.  
PR 08-APR-2001; 2001US-0282121P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
XX Baughn WR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
PI Kallick DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;  
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee EA, Harland L;  
XX  
XX WPI; 2002-627557/57.  
DR P-PSDB; AAB71327.  
XX  
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
XX Claim 115; Page 213-214; 239pp; English.  
XX  
XX This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
CC hepatotropic, laxative, cerebrotrophic, antinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GCREC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-  
CC AAB71369, described in the disclosure of the invention  
XX  
SQ Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1.27e-128 Length: 1460  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
  
US-10-055-106c-2 (1-305) x AAF88585 (1-1460)  
  
Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
Db 343 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGATCCTATAGTACACCCACTTA 402  
Qy 21 IleSerLeuTyrPheIleValleuIleGlyLeuValGlyValIleSerLeuPhe 40  
Db 403 ATCAGCCTCTACTTCATAGTGTATTATGGCGGCTGGTGGTGTTCATTTCCATTTCTTTC 462  
Qy 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
Db 463 CTCCTGGTGAATGAATGACACCCGGTCAGTACACCATCGCGGTCTATTAACTTGGTGGTG 522  
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysThr 80  
Db 523 GTCCACAGGGTTTTCTGTGTCAGTGCATTTGCGCTTGACCTATCATCAAGAAGACT 582  
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisMetTyr 100  
Db 583 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGGAGTGGCCATGCTGCACATGACATGTAC 642  
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120

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399 GTCCACAGCGTTTCTGCTGAGAGTCCATTTGCTTACCTACCTACCAAGACT 458
81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisTyr 100
459 TGGATGTTGGGCTGCGCTTCTCAAAATTTGTAGTGCCATGTCACATCCACATGTAC 518
101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
519 CTCACGTTCTCTATCTATGTTGGTGATCCTGCTCACCAGATACCTCATCTTCTCAAGTGC 578
121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
579 AAAGACAAAGTGAATCTTACAGAAACTGCATGCTGGCTGCCAGTCTGGCATGTGG 638
141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
639 ACCTGCTGATGTTGATGTTGGTACCCCTGTTGCTCCGGTATGGATCCATGAGGA 598
161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
699 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 758
181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
759 ATCACTATATGATGATCATTTTGTGATAGCCGTTGCTGTGATTCGTGTTCTCCAG 818
201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
819 GTCTTCATCATATTGTTGATGTTGCAGAGCTACGCCACTCTTTACTATCCACAGAG 878
221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
879 TTCGTGGCTCAGCTGAAACCACTATTATTTATAGGGGTCACTCTGTTTGTTCCTTCCC 938
241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
939 TACCAGTCTCTTGGAGTCTATTACTTGAATGTTGTGACGCAATCCATGCTGTAAACAG 998
261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
999 AAGGTTGCAATTTTATAACGAAATCTTTCTTGAGTGTAAACGCAATTAAGCTGATGTTG 1058
281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTrpAsn 300
1059 CTTCCTCTTGTCTTTGGGGAGCCATTTGTTTAAACAAAGATAATTGGCTTATGGAT 1118
301 CysValLeuCysArg 305
1119 TGTGTTTGTGCGGT 1133
RESULT 8
ID AAF88584 standard; cDNA; 1340 BP.
XX AAF88584;
AC AAF88584;
XX 19-NOV-2002 (first entry)
XX Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytotatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection;
XX gene therapy; gene; ss.
XX Homo sapiens.
XX WO200263004-A2.
XX 15-AUG-2002.
PD
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XX 06-FEB-2002; 2002WO-US003635.
XX 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX (INCY-) INCYTE GENOMICS INC.
PA Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
XX Kallick DA, Gandhi AR, Wallia NK, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX WPI; 2002-627557/67.
DR P-PSDB; AAB71326.
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX Claim 114; Page 213; 239pp; English.
XX This invention describes novel polypeptides which have anti-HIV,
XX antiarteriosclerotic, cytotatic, neuroprotective, antiparkinsonian,
XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
XX antibacterial, fungicide and protozoacide activity. The products of the
XX invention are useful for treating a disease or condition associated with
XX decreased expression or over expression of functional G-protein coupled
XX receptors (GCREC), while antibodies generated against the polypeptide of
XX the invention are useful for diagnosing a condition or disease associated
XX with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
XX The compounds described in the invention can be used for gene therapy.
XX AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-
XX AAB71369, described in the disclosure of the invention
SQ Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.15e-128 Length: 1340
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AAF88584 (1-1340)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
DB 223 ATGCCTGGCCACAATACCTCCAGGAATTCCTTTGGATCCTATAGTGACACCCACTTA 282
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 283 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATCTTTTC 342
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 343 CTCCTGGTGAATGAACACCCCGCTCAGTGACCACTGCGGTCAATTAATTTGGTGTG 402
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLeuThr 80
DB 403 GTCCACAGCGTTTTTCTGCTGACAGTGCCTATTTGCTTGACCTCATCAAGAGACT 462
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
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Db 180 CTCCTGGTGAATAACACACCGGTCAGTGACCCACATGGCGGTCAATTAACATTTGGTGTG 239
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleIleValThr 80
Db 240 GTCCACACGCTTTTCTCTGACAGTGCATTTGCTTGACCTACCTACCTCATCAAGAAGACT 299
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 300 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 359
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 360 CTCACGTTCTTATCTATGTGTGTATCTCTGTCACCATACCTCATCTCTTCAAGTGC 419
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 420 AAAGCAAGTGGAAATTTCTACAGAAACTGATGCTGTGGTGCAGCTGCTGGCATGTGG 479
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 480 ACGCTGGTGATTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
QY 161 TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 540 TACAATGAGGAGCACTGTTTAAATTTTCAAGAGCTTGCTTACACATATGTGAAATC 599
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 600 ATCAACTATATGATAGTATCTTTTGTATAGCCGTTGCTGCTGCTGCTGCTGCTGCTG 659
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 660 GTCTTCATCATATGTTGATGGTGAGAGCTAGCCCACTCTTTACTATCCACACGAG 719
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 720 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTTGTTTCTTCCC 779
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 780 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGAGCGCATTCATGCTGTAAACAGC 839
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 840 AAGGTGCAATTTTATACCAATATTTCTTGAGTGTACAGCAATGCTGCTATGATTG 899
QY 281 LeuLeuPheValPheGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db 900 CTTCCTTTGCTTTGGGGGAAGCATTTGTTTAAAGCAAAAGATAATTTGCTTATGGAAT 959
QY 301 CysValLeuCysArg 305
Db 960 TGTGTTTGTCCCGT 974
RESULT 7
AAF88583
ID AAF88583 standard; cDNA; 1336 BP.
AC AAF88583;
XX
DT 19-NOV-2002 (first entry)
XX
DE Human GCREC-4 cDNA INCYTE ID 90012430CD1 SEQ ID 52.
XX
KW GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
```

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XX PN WO200263004-A2.
XX PD 15-AUG-2002.
XX PF 06-FEB-2002; 2002WO-US003635.
XX PR 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX (INCY-) INCYTE GENOMICS INC.
XX Baughn WR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AK, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX MPI; 2002-627557/67.
DR P-PSDB; AAB71325.
XX
PT New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX
PS Claim 113; Page 212-213; 239pp; English.
XX
CC This invention describes novel polypeptides which have anti-HIV,
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or over expression of functional G-protein coupled
CC receptors (GCREC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAF88580-AAF88527 encode the GCREC proteins represented by AAB71322-
CC AAB71369, described in the disclosure of the invention
XX
SQ Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.15e-128 Length: 1336
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AAF88583 (1-1336)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 219 ATGCCTGGCCACAATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 278
QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 279 ATCAGCTCTACTTCAATAGTCTTATTGGCGGGTGGTGGTGCATTTCCATCTTTTC 338
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 339 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCACTGCGGTGCATTAACATTTGGTGTG 398
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
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QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
 DB 121 CTCCTGGTGAATATGAAACACCGGTCAGTGACCACCTGGGGTCATTAACTTGGTGGT 180  
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80  
 DB 181 GTCCACAGCGTTTCTCTGTGACAGTGCATTTCTGCTGACCTACCTCATCAAGAAGACT 240  
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
 DB 241 TGGATGTTTGGCTGCCCTCTGCAAAATTTGAGTGCCATGCTGCACATCCATGATGAC 300  
 QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
 DB 301 CTCACGTTCTATTCTATGTGGTGATCTCTGGTCACCATACCTCATCTTCTCAAGTGC 360  
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAspAlaGlyMetTrp 140  
 DB 361 AAAGCAAGTGAATTTCTACAGAAATTCGATGCTGGCTGCCAGTGGCATGTGG 420  
 QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
 DB 421 ACGCTGGTGATGTTCATTTGTGTACCCCTGGTTGTCTCCGCTATGGAATCCATGAGAA 480  
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
 DB 481 TACAAATGAGGACACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540  
 QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
 DB 541 ATCACTATATGATAGTATCATTTTGTCTATAGCCGTTGCTGTGATTTCTTGGTCTTCCAG 600  
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 DB 601 GTCTTCATCATTTATGATGTGAGAGCTACGCCACTCTTTACTATATCCACAGAG 660  
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPheIleGlyValIleLeuValCysPheLeuPro 240  
 DB 661 TTCGGGCTGCTGAAACCACTATTTTATAGGGTCATCCCTGTGTGTTCTTCTTCCC 720  
 QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
 DB 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTGTGACGCCATTCCAATGCCCTGTAAACAGC 780  
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 DB 781 AAGGTTCATTTTATACGAAATCTTCTTGAGTGTPACAGCAATTAGCTGCTATGATTG 840  
 QY 281 LeuLeuPheValPheGlyCysSerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
 DB 841 CTTCTCTTTGCTTTGGGGAGCCATTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
 QY 301 CysValLeuCysArg 305  
 DB 901 TGTGTTTGTGGCGT 915  
 RESULT 5  
 AAL57070  
 ID AAL57070 standard; DNA; 1040 BP.  
 XX  
 AC AAL57070;  
 XX  
 DT 17-SEP-2003 (first entry)  
 XX  
 DE Human G-protein coupled receptor GAVE18 DNA sequence.  
 KW Human G-protein coupled receptor; GAVE18; signal transduction;  
 KW inflammation; physiological immunological response; anti-inflammatory;  
 KW antiasthmatic; antirheumatic; antiarthritic; antitense therapy;  
 KW chromosomal mapping; tissue typing; forensic biology;  
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;  
 KW rheumatoid arthritis; gene; ds.

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 1..918  
 FT /\*tag= a  
 FT /product= "GAVE18 protein"  
 XX  
 FN WO2003042399-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US035887.  
 XX  
 PR 13-NOV-2002; 2001US-0354150P.  
 PR 22-MAR-2002; 2002GB-00006891.  
 XX  
 PA (AVET ) AVENTIS PHARM INC.  
 XX  
 PI Eisingdrelo H, Cai J, Busch SJ, Gassenhuber J;  
 XX  
 DR WPI; 2003-457496/43.  
 DR P-PSDB; AAO27265.  
 XX  
 FT New GAVE18 polypeptide and nucleic acid molecule encoding the  
 PT polypeptide, useful for preventing and treating a disease or disorder  
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or  
 PT rheumatoid arthritis.  
 XX  
 PS Claim 1; Fig 5; 89pp; English.  
 XX  
 CC This invention relates to a novel G-protein coupled receptor (GAVE18)  
 CC that is involved in signal transduction in respect to inflammation and  
 CC the physiological immunological response. Molecules which may modulate  
 CC the signalling activity or signal transduction of the receptor may be  
 CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The  
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for  
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18  
 CC proteins and antibodies may be useful in screening assays, detection  
 CC assays (for example chromosomal mapping, tissue typing or forensic  
 CC biology), or predictive medicine (for example diagnostic assays.  
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The  
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse  
 CC agonist and antagonist are also useful for preventing and treating a  
 CC disease or disorder associated with aberrant expression or activity of  
 CC GAVE18, such as inflammation and immunological-related diseases or  
 CC disorders, for example asthma, chronic obstructive pulmonary disease or  
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding  
 CC the GAVE18 protein of the invention  
 XX  
 SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8, 65e-129 Length: 1040  
 Score: 1552.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-055-106C-2 (1-305) x AAL57070 (1-1040)  
 QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20  
 DB 1 ATGCCTGGCCACAATACCTCCAGAAATTCCTCTTGGCATCTATAGTACACCCCACTTA 60  
 QY 21 ILeSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40  
 DB 61 ATACGCTCTACTTTCATAGTCTTATTTGGCGGCTGGTGGGTGTCATTTCATCTTTTC 120  
 QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
 DB 121 CTCCTGGTGAATATGAAACACCGGTCAGTGACCACCTGGCGGTCACTTAACCTGGTGGT 180

DB: 6 Gaps: 0  
US-10-055-106C-2 (1-305) x ABZ59171 (1-918)  
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20  
Db 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTGGGATCCTATAGTGACACCCACCTTA 60  
QY 21 IleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40  
Db 61 ATCAGCCTCTACTTCTATAGTGTCTATTTGGGGCTGGTGGTGTCTATTTCCATTCTTTTC 120  
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60  
Db 121 CTCCTGGTGAATGAAACACCCGGTCAGTGACACCACTGGCGTCAATTAACCTGGTGG 180  
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrThrLeuIleLysIleThr 80  
Db 181 GTCCACAGCGTTTTCTGCTGACAGTGCCATTTTCGTTGACCTACCTCATCAAGAGACT 240  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetIleHisIleHisMetTyr 100  
Db 241 TGGATGTTGGGTGGCTCTGCAATTTGTGAGTGCCATGTCGACATCCACATGATGAC 300  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
Db 301 CTCACGTTCTATTCTATGTGTGTGATCTGTCCTGTCACCAAGATCTCTCTTCAAGTGC 360  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140  
Db 361 AAGACAAAGTGAATTTCTACAGAAATGTCATGCTGTGGTGCCAGTCTGGCATGTGG 420  
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
Db 421 ACCTGGTGAATGATCTGT 480  
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIle 180  
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAGAGCTTGTCTTACACATATGTGAATTC 540  
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
Db 541 ATCACTATATATGATGATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
Db 601 GTCTTCATCATATTATGT 660  
QY 221 PheTyrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
Db 661 TTCTGGCTCAGCTGAAACACCTATTTTATAGGGGTCTATCTTTGTTGTTCTCTTCC 720  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
Db 721 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTACAGC 780  
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
Db 781 AAGTTGCAATTTTATACGAAATCTCTTGTGAGTGAACAGCAATTAAGTCTATGATTGG 840  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleLeuGlyLeuTrpAsn 300  
Db 841 CTTCCTCTTCTCTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
QY 301 CysValLeuCysArg 305  
Db 901 TGTGTTTTGGCGT 915  
RESULT 4  
ABZ59171  
ID ABZ59171 standard; DNA; 918 BP.  
XX  
AC ABZ59171;

XX DT 28-APR-2003 (first entry)  
XX DE Human TGR343 protein encoding DNA.  
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;  
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;  
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;  
KW immunosuppressive; antiinflammatory; gene; ds.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FH 1. 918  
CDS /\*tag= a  
FT /product= "TGR343"  
FT  
XX WO2003004678-A2.  
XX 16-JAN-2003.  
XX 01-JUL-2002; 2002WO-US020860.  
XX 03-JUL-2001; 2001US-0302800P.  
XX (TULA-) TULARIK INC.  
XX Tian H, Dai K, Chen J, Zhao J, Cutler G;  
XX WPI; 2003-210368/20.  
XX P-PSDB; ABP71378.  
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
PT nephrolithiasis.  
XX Claim 7; Page 61; 74pp; English.  
XX The invention provides new G-protein coupled receptor (GPCR) polypeptides  
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding  
CC polynucleotides. The polypeptides can be expressed by standard DNA  
CC recombination methodology. The polypeptides are useful for screening or  
CC identifying modulation of GPCR or signal transduction. The modulators of  
CC signal transduction are useful for treating or preventing TGR-associated  
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
CC polypeptides are useful as targets for diagnosing or treating e.g.  
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,  
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute  
CC inflammatory dermatoses. The present sequence represents a human TGR343  
CC protein encoding DNA  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.52e-129 Length: 918  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0  
US-10-055-106C-2 (1-305) x ABZ59171 (1-918)  
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20  
Db 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTGGGATCCTATAGTGACACCCACCTTA 60  
QY 21 IleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40  
Db 61 ATCAGCCTCTACTTCTATAGTGTCTATTTGGGGCTGGTGGTGTCTATTTCCATTCTTTTC 120

CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA  
 CC libraries from peripheral blood mononuclear cells. Two ESTs have been  
 CC identified in libraries derived from breast mRNA. PFI-021 and the  
 CC corresponding cDNA are used to treat a patient needing altered activation  
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,  
 CC neurology, psychology, urogenital disease, reproductive and sexual  
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin  
 CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic  
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-  
 CC infection, sensory organ disorders, sleep disorders and hair loss  
 XX  
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,52e-129 Length: 918  
 Score: 1592.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x ABA00160 (1-918)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
 DB 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTCGGATCCTATAGTGACACCCACTTA 60  
 QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
 DB 61 ATCAGCCCTACTTCATAGTGTCTATTGGCGGCTGTGGTGTCAATTCCTATTCCTTTTC 120  
 QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
 DB 121 CTCCTGGTGAATGAACACCCGTCAGTACCCATCCAGCGGTCAATTAATTCCTGGTG 180  
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLeuThr 80  
 DB 191 GTCCACACGGTTTCTGCTGCACAGTGCATTCCTGCTTACCTCATCAAGAGACT 240  
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
 DB 241 TGGATGTTTGGCTGCCCTCTCGAAATTTGTGAGTGCATGCTGCACATCCATGATGAC 300  
 QY 101 LeuThrPheLeuPheTyrValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
 DB 301 CTCAGTTCCTATCTATGTTGGTGATCTGCTGCACAGATACCTCATCTTCTCAAGTGC 360  
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLaserAlaGlyMetTrp 140  
 DB 361 AAAGACAAAGTGAATTCACAGAAACTGCATGCTGTGGTGCAGTGCCTGGCATGTGG 420  
 QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
 DB 421 ACGCTGGTGAATGTCATGTTGTGATCCCTGTTGTCCTCCGGTATGGATCATGAGAA 480  
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
 DB 481 TACATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAATC 540  
 QY 191 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
 DB 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTCTGCTTCCAG 600  
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 DB 601 GTCITTCATCATATGTTGATGTTGTGAGAGCTACGCCACTCTTTACTATCCACAGGAG 660  
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
 DB 661 TTCCTGGTCACTGAGTGAACACCTATTTTATAGGGGTCACTCTGTTGTTCTCTCC 720  
 QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260

DB 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATCCCTGTACAGC 780  
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 DB 781 AAGTTGCAATTTTATACGGAATCTCTTGTAGTGTATACAGCAATTAGCTGCTATGATTG 840  
 QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
 DB 841 CTCTCTCTTTGCTCTTGGGGAGCCATTGTTTAAAGCAAAAGATAATTCGCTTATGGAAT 900  
 QY 301 CysValLeuCysArg 305  
 DB 901 TGTTTTTTGGCCGT 915

RESULT 3  
 ABT04867  
 ID ABT04867 standard; cDNA; 918 BP.  
 AC ABT04867;  
 XX  
 DT 11-OCT-2002 (first entry)  
 XX  
 DE Human G protein coupled receptor hRUP29 coding sequence.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;  
 KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200242461-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 26-NOV-2001; 2001WO-US044386.  
 XX  
 PR 27-NOV-2000; 2000US-0253404P.  
 PR 12-DEC-2000; 2000US-0255366P.  
 PR 20-FEB-2001; 2001US-0270266P.  
 PR 20-FEB-2001; 2001US-0270266P.  
 PR 06-APR-2001; 2001US-0282032P.  
 PR 06-APR-2001; 2001US-0282356P.  
 PR 06-APR-2001; 2001US-0282358P.  
 PR 06-APR-2001; 2001US-0282365P.  
 PR 14-MAY-2001; 2001US-0290917P.  
 PR 31-JUL-2001; 2001US-0309208P.  
 XX  
 PA (AREN-) ARENA PHARM INC.

XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;  
 XX  
 XX WPI; 2002-566565/60.  
 XX P-PSDB; ABJ04069.  
 XX  
 XX Novel endogenous and non-endogenous versions of G protein-coupled  
 XX receptor useful for identification of candidate compounds as receptor  
 XX agonists or antagonists for use as therapeutic agents.  
 XX  
 XX Claim 7; Page 56-57; 84pp; English.

XX The present invention provides the protein and coding sequences of  
 XX several human G-protein coupled receptors (GPCRs). These can be used in  
 XX the identification of candidate compounds as receptor agonists or inverse  
 XX agonists having applicability as therapeutic agents. The present sequence  
 XX is a GPCR coding sequence of the invention  
 XX  
 XX Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,52e-129 Length: 918  
 Score: 1592.00 Matches: 305  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0

(TAKE ) TAKEDA CHEM IND LTD.

Moriya T, Ito T, Shintani Y, Miyajima N;

WPI; 2002-098071/13.

P-PSDB; AAM48989.

Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat e.g. diseases of central nervous system, inflammations and diseases of circulatory system.

Claim 5; Page 99; 110pp; Japanese.

The present invention provides the protein and coding sequences of a novel human testis-originated G protein-coupled receptor protein TGR10. The sequences can be used in the development of drugs for the treatment of diseases of the central nervous system, inflammations, diseases of the circulatory system, cancer, metabolic diseases, immunological diseases, and diseases of the gastrointestinal system. The present sequence is the coding sequence of the invention

Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 7,52e-129 Length: 918  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x AAL44713 (1-918)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
DB 1 ATGCCTGGCCACATACCTCCAGGAATCTCTTGGATCCTATAGTACACCCACTTA 60  
QY 21 IleSerLeuThrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 61 ATCAGCCTCTACTTATAGTGCCTATTATGGGGGCTGGTGGTGTCTATTCATTCTTC 120  
QY 41 LeuLeuValIleMetAsnThrArgSerValThrThMetAlaValIleAsnLeuVal 60  
DB 121 CTCTGTGTGAATGAACACCCGGTCACTAGTACACCATGCGGTCTATTAATTTGGTGG 180  
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysThr 80  
DB 181 GTCCACAGCGTTTCTCTGTGACAGTGCCTATTCGGCTTGACCTACCTCATCAAGAAG 240  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCATGTAC 300  
QY 101 LeuThrPheLeuPheTyrValIleValIleLeuValThrArgTyrLeuIlePheLysCys 120  
DB 301 CTCACGTTCTCTATGTATGGTGATCTCTGACACAGATACCTCATCTTCTTCAAGTGC 360  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaIleAsnAlaGlyMetTrp 140  
DB 361 AAAGACAAATGGGAATTTCTACAGAAATCTGATGCTGTGGTGCCTGCTGCATGTGG 420  
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
DB 421 ACCTGTGTGATGTCTATGTGGTACCCCTGTTGTCCTCCGGTATGGAATCCATGAGAA 480  
QY 161 TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
DB 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAATTC 540  
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
DB 541 ATCAACTATATGATAGTCAATTTTGTGATACCGCTGCTGTGATCTGTGGTCTCCAG 600

QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
DB 601 GTCTTCATCATATATGTGATGGTGCAGAGCTAGCCACTCTTTTACTATCCACAGAG 660  
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
DB 661 TTTGGGCTCAGCTGAAAACCTATTTTATAGGGTCACTCTTGTTCCTTCCC 720  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
DB 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGATTCATCAATGCTGAAACG 780  
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
DB 781 AAGTTGCAATTTTATACGAATCTCTTGTAGTGTAAACAGCAATAGCTGTATGATTG 840  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300  
DB 841 CTCTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGCTTATGGA 900  
QY 301 CysValLeuCysArg 305  
DB 901 TGTGTTTGTGCGGT 915  
RESULT 2  
ABA00160  
ID ABA00160 standard; cDNA; 918 BP.  
AC ABA00160;  
XX  
DT 15-NOV-2002 (first entry)  
DE PFI-021 cDNA.  
KW Gene; human; G-protein coupled receptor; GPCR; PFI-021;  
KW peripheral blood mononuclear cell; BMC; breast; inflammation; allergy;  
KW respiratory; neurology; psychology; urogenital disease;  
KW reproductive dysfunction; sexual dysfunction; cancer; tissue repair;  
KW dermatology; skin pigmentation; photoaging; frailty; osteoporosis;  
KW metabolic disease; cardiovascular disease; sleep disorder; hair loss;  
KW gastrointestinal disease; anti-infection; sensory organ disorder; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..918  
FT /\*tag= a  
FT /product= "PFI-021"  
XX  
EP1225183-A2.  
XX  
PD 24-JUL-2002.  
XX  
PF 09-JAN-2002; 2002EP-00250128.  
XX  
PR 23-JAN-2001; 2001GB-00001739.  
XX  
PA (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX  
PI Harland L;  
XX  
DR WPI; 2002-601226/65.  
DR P-PSDB; AAG79446.  
XX  
PT New human G-protein coupled receptor involved in signal transduction,  
PT useful to treat disorders associated with its expression or activity such  
PT as inflammation, allergy and cancer.  
PS Claim 1; Fig 1; 8pp; English.  
XX  
CC This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 25, 2004, 18:01:50 ; Search time 447 Seconds  
(without alignments)  
2898.859 Million cell updates/sec

Title: US-10-055-106C-2  
Perfect score: 1592  
Sequence: 1 MFGHTSRNSSCDPVTTPHL.....GGSHWFKQKIGLWNCVLCR 305

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: Geneseqn2001bs:.\*  
6: Geneseqn2002as:.\*  
7: Geneseqn2002bs:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1592	100.0	918	AAL44713	Aal44713 Human tes
2	1592	100.0	918	ABA00160	ABA00160 PFI-021 c
3	1592	100.0	918	ABT04867	ABT04867 Human G p
4	1592	100.0	918	ABZ59171	ABZ59171 Human TGR
5	1592	100.0	1040	AAL57070	Aal57070 Human G-p
6	1592	100.0	1051	ABX87351	ABX87351 Human CDN
7	1592	100.0	1336	Aaf88583	Aaf88583 Human GCR
8	1592	100.0	1340	Aaf88584	Aaf88584 Human GCR

9	1592	100.0	1460	6	AAP88585	Human GCR
10	1592	100.0	2525	4	AAH51009	Human nGP
11	1592	100.0	2525	6	ABS70242	DNA encod
12	1592	100.0	113306	9	ADC86554	Human GPC
13	1587	99.7	939	6	AAL53414	939 nt co
14	1587	99.7	1684	6	AAL53413	1684 nt c
15	1547	97.2	1499	6	AAD37670	Human G-p
16	1176	73.9	972	9	ADC12789	Human GPC
17	1141	71.7	810	9	ADB78584	Mouse G-p
18	674	42.3	447	4	AAH50979	Human nGP
19	674	42.3	447	6	ABS70212	DNA encod
20	538	33.8	897	7	ABZ23663	G protein
21	294	18.5	479	4	AAK56763	Human imm
22	250	15.7	1358	3	AAZ95038	Human G p
23	247	15.5	1014	4	AAD06501	Human CYS
24	247	15.5	1014	7	ABZ42532	Human CON
25	245	15.4	1119	9	ADB74248	Rat GPR34
26	245	15.4	1122	9	ADB74249	Rat GPR34
27	240	15.1	1578	2	AAV62388	Human 7-t
28	240	15.1	1578	2	AAV71117	Mouse GPR
29	236	14.8	1125	9	ADB74251	Mouse GPR
30	232.5	14.6	1498	4	AAH47235	Human C-p
31	232.5	14.6	1498	4	AAH16527	Human CDN
32	232	14.6	1101	4	AAF81543	Pig LNC4
33	231.5	14.5	1077	4	AAF82359	Human G p
34	231.5	14.5	1077	4	AAF86985	Human nov
35	231.5	14.5	1077	4	AAF55101	Nucleotid
36	231.5	14.5	1077	7	ACC51022	Human bla
37	231.5	14.5	1104	7	AAD52811	Human Mow
38	231.5	14.5	1143	9	ADB74230	Human GPR
39	231.5	14.5	1146	2	AAV61053	Human CLO
40	231.5	14.5	1146	7	ABZ42812	Human G p
41	231.5	14.5	1164	4	AAD06508	Human CON
42	231.5	14.5	1402	6	AAZ98046	Human DNA
43	231.5	14.5	1402	7	ABX76412	Lung canc
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ALIGNMENTS

RESULT 1

AAL44713  
ID AAL44713 standard; DNA; 918 BP.

XX AAL44713;

XX 03-MAY-2002 (first entry)

DT Human testis originated G-protein coupled receptor TGR10 coding sequence.

DE Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;

KW cystostatic; immunomodulator; cardiac; neuroprotective; gene therapy;

KW inflammation; nervous system disease; circulatory system disease; cancer;

KW metabolic disease; immunological disease; gastrointestinal disease; gene;

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS i. 918

FT /tag= a

FT /product= "TGR10"

XX WO200196567-A1.

XX PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-JF005061.

XX PR 15-JUN-2000; 2000JP-00184596.

XX PR 19-JUL-2000; 2000JP-00233887.

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Db	861	TACAATGAGGACACTGTTTAAATTCACAAAGAGCTTGCTTACACATATGTGAAATC	920
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln	200
Db	921	ATCAACTATATATATAGTCAATTTTGTATAGCGTGTGCTGATTCCTGTTGGTCTTCCAG	980
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220
Db	981	GTCCTTCATCATTTATGTATGTGTGAGAGCTACGCCACTCTTTACTATCCACCAGGAG	1040
QY	221	PheTrpAlaGlnLeuLysAsnLeuPheIleGlyValIleLeuValCysPheLeuPro	240
Db	1041	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGTCATCCTTGTTGTTCTTCTCC	1100
QY	241	TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer	260
Db	1101	TACCAGTTCCTTTAGGATCTATTACTTGAATGTGTGAGCATTCCAATGCCCTGTAAACAGC	1160
QY	261	LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAsnLeu	280
Db	1161	AAGGTGTCATTATTAACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGCTATGATTG	1220
QY	281	LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn	300
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QY	301	CysValLeuCysArg	305
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Search completed: April 25, 2004, 21:29:30  
Job time : 4525 secs

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Percent Similarity: 99.34% Conservatives: 0
Best Local Similarity: 99.34% Mismatches: 2
Query Match: 99.18% Indels: 0
DB: 2 Gaps: 0

US-10-055-106c-2 (1-305) x AC146385 (1-164055)

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QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 16061 ATCAGCCTCTACITCATAGTGCTCATTTGGGGGCTGGTGGTGCATTTCCATCTTTTC 16002
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal 60
DB 16001 CTCCTGGTGAATAATGACACCCGCTCAGTGACCACTGGCGGTCAATTAACCTTGGTGGTG 15942
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
DB 15941 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAGAGACT 15882
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 15881 TGGATGTTGGGCTGCCCTCTGCAAAATTTCTGAGTGCCATGCTGCACATCCACATGTAC 15822
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 15821 CTCACGTTCTATCTAATGGTGATCCTGTCACAGATACCTCACTTCTTTCATAGTGC 15762
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLysAlaGlyMetTyr 140
DB 15761 AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGGTGGCTGCCAGTGGCATGTGG 15702
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 15701 ACCTGGTGATGTGTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 15642
QY 161 TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 15641 TACAAAGAGGACACTGTTTACATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 15582
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 15581 ATCAACTATATGATAGTCATTTTGTATAGCCGTTGCTGTGATCTGTTGGTCTTCCAG 15522
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 15521 GTCTTCATCATATTATGTTGATGGTGCAGAGCTACGCCACTCTTACTATCCACAGGAG 15462
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 15461 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCCTGTTGTTTCTTCTCC 15402
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 15401 TACAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGATTCCTCAATGCTCTGACAGC 15342
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 15341 AAGGTTCAATTTATAACGAAATCTTCTGAGTGTACAGCAATAGCTCTATGATTG 15282
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
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DB 15281 CTTCTCTTTGCTTTGGGGAGCCATTGGTTTAAACAAAAGATAATTGACTTATGGAAT 15222
QY 301 CysValLeuCysArg 305
DB 15221 TGTGTTTGTGCCGT 15207

RESULT 15
AX451925 1499 bp DNA linear PAT 03-JUL-2002
LOCUS AX451925
DEFINITION Sequence 22 from Patent WO0226825.
ACCESSION AX451925
VERSION AX451925.1 GI:21698748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Baughn,M.R., Graul,R.C., Walla,N.K., Gandhi,A.R., Hafalia,A.J.,
Ramkumar,J., Tribouley,C.M., Thornton,M., Kallick,D.A., Yao,M.G.,
Elliot,V.S., Burford,N., Khan,F.A., Yue,H., Lu,Y., Arvizu,C.,
Roopa,R., Nguyen,D.B., Lee,E.A., Lu,D.A., Ison,C.H., Walsh,R.T. and
Policky,J.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226825-A 22 04-APR-2002;
INCYTE Genomics, Inc. (US)
FEATURES
source
1. 1499
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Score: 1547.00 Matches: 303
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Best Local Similarity: 99.34% Mismatches: 2
Query Match: 97.17% Indels: 2
DB: 6 Gaps: 0

US-10-055-106c-2 (1-305) x AX451925 (1-1499)

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QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 441 ATCAGCCTCTACTTCTATAGTGTCTTATTTGGCGGGTGGTGGTGTCTTCCATTTCTTTC 500
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal 60
DB 501 CTCCTGGTGAATAATGAACACCCGCTCAGTGACCACTGGCGGTCAATTAACCTTGGTGGTG 560
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
DB 561 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTGACCTCTCATCAAGAGACT 620
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 621 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 680
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 681 CTCAGTCTCTATTCTATGTGTGATCTCTGTACCATACCTCATCTTCTTCAAGTGC 740
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLysAlaGlyMetTyr 140
DB 741 AAAGACAAAGTGAATTTCTACAGAAACTGTCATGCTGTGGTGGCTGCCAGTGTGGCATGTGG 800
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Alignment Scores:
Pred. No.: 1.97e-108 Length: 218186
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
DB 133183 ATCAGCCTCTACTTCATAGTCTATTGGCGGCTGGTGGGTGCATTTCCATTCTTTTC 133242
QY 41 LeuLeuValIleMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 133243 CTCCTGTGCAAAATGAACACCCGGTCAGTGACACCATCGCGGTCAATAACTTGGTGGTG 133302
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLeuLysLysThr 80
DB 133303 GTCCACAGCGTTTCTGCTGACAGTGCCATTTCGCTTGACCTACTCATCAAGAAGACT 133362
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 133363 TGGATGTTTGGGTGCGCTCTCTGCAATTTGTGAGTGCCATGTCACATCCACATGTAC 133422
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 133423 CTCACGTTTCTATTCTATGTTGATCCTGTCACAGATACCTCATCTTCTTCAAGTGC 133482
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
DB 133483 AAAGACAAAGTGAATTTCTACGAAACTGCATGCTGTGGCTGCCAGTCTGCCATGTGG 133542
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 133543 ACCTCGTGAATGTCATTTGTTGTTACCCCTGGTTGTCTCCGGTATGGAATCATCAGGNA 133602
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 133603 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 133662
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 133663 ATCAACTATATGATGATCATTTTGTGATAGCCGTTGCTGTGATTCGTGTGCTTCCAG 133722
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
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QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 133783 TTCTGGGCTCAGATGAAACCTATTTTATAGGGGTGCATCTGTTGTTCTTCTTCC 133842
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 133843 TACCAGTTCTTAGGATCTATTACTTGAATGTTGTGACGCAATTCCAATGCTGTAAACAG 133902
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 133903 AAGGTTGCATTTTATACGAAATCTTCTTGAAGTGAACGCAATAGCTGCTATGATTG 133962
QY 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTrpAsn 300
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QY 301 CysValLeuCysArg 305
Db 134023 TGTGTTTTTGCCGT 134037

RESULT 14
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LOCUS Pan troglodytes chromosome UNK clone Rp43-126C6, *** SEQUENCING IN
DEFINITION PROGRESS ***, 3 unordered pieces.
ACCESSION AC146385 GI:38154073
VERSION AC146385.2 GI:38154073
KEYWORDS HTG; HTGS PHASE1.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 164055)
AUTHORS Wilson,R.K.
TITLE The sequence of Pan troglodytes clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164055)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 164055)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Nov 4, 2003 this sequence version replaced gi:33620890.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: C_P126C06
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162205 bases at least Q40
Consensus quality: 162489 bases at least Q30
Consensus quality: 162744 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 24885: contig of 24885 bp in length
* 24886 24985: gap of unknown length
* 24986 65573: contig of 41588 bp in length
* 65574 164055: gap of unknown length
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## Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

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Db 11720 GTCCACAGCGTTTTCTGCTGACAGTCCCATTTGCTTACCTTACCTCATCAGAGACT 11779
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Db 11780 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 11839
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Db 11900 AAGACAAAGTGAATCTACAGAAATGCTATGCTGGTCCAGTCTGCATGCTGGCATGG 11959
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QY 261 LysValAlaPheTyrlAsnGluIlePheLeuSerValThrAlaIleSerCysTyrlAspLeu 280
Db 12320 AAGTTTCATTTTATACGAAATCTCTTCTGAGTGTACAGCAATTAGCTGCTATGATTG 12379
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheGlyGlnLysIleLeuGlyLeuTrpAsn 300
Db 12380 CTTCTCTCTTGTCTTGGGGGAAGCATTGCTTTAAGCAAAAGATAATTGGCTTATGGAAT 12439
QY 301 CysValLeuCysArg 305
Db 12440 TGTGTTTGTGCGT 12454

RESULT 13
AC083865 218186 bp DNA linear PRI 26-JAN-2001
LOCUS Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
DEFINITION AC083865
ACCESSION AC083865.2 GI:12545315
VERSION AC083865.2
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 218186)
AUTHORS Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
TITLE Large-scale Mapping and Sequencing of Human Chromosome 7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 218186)
AUTHORS Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.E.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 218186)
AUTHORS Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgss@u.washington.edu
----- Project Information
Center project name: HsaChr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator Em-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217693 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-fp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': mapping in progress
3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap
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QY 181 ILeAsnTyrMetIleValIlePheValIleAlaValIleLeuLeuValPheGln 200  
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QY 201 ValPheIleIleMetLeuMetValGlnIlyValLeuArgHisSerLeuLeuSerHisGlnGlu 220  
DB 627 GTCTTCATCATATGTTGATGTTGTCAGAGAGTACGCCACTCTTTACTATCCACACAGAG 686  
QY 221 PheTrpAlaGlnLeuLeuAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
DB 687 TTCTGGGTCAGTCGAAACCTATTTTATAGGGTCACTCTTGTGTTTCTTCCTTCCTCC 746  
QY 241 TyrGlnPhePheArgIleTyrTrpLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
DB 747 TACCAGTTCCTTTAGGATCTTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 806  
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
DB 807 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTGTATGATTG 866  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheGlyGlnIlyLeuIleGlyLeuTrpAsn 300  
DB 867 CTCTCTCTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926  
QY 301 CysValLeuCysArg 305  
DB 927 TGTGTTTGTGCGGT 941  
RESULT 11  
AX521885 2525 bp DNA linear PAT 24-OCT-2002  
LOCUS Sequence 81 from Patent WO02064789.  
DEFINITION AX521885  
ACCESSION AX521885  
VERSION AX521885.1 GI:24410791  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Lind, P., Parodi, L.A., Vogeli, G. and Wood, L.S.  
G protein-coupled receptor  
Patent: WO 02064789-A 81 22-AUG-2002;  
PHARMACIA & UPJOHN COMPANY (US)  
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/mol\_type="unassigned DNA"  
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Alignment Scores:  
Pred. No.: 2,71e-110 Length: 2525  
Score: 1592.00 Matches: 305  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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DB 27 ATGCTGCGCCAAATACCTCCAGGAATTCCTCTTCGATCCCTATAGTGACCCACCTTA 86  
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 87 ATCAGCCTCTACTTCATAGTGTATTTGCGGGCTGGTGGGTGCTCATTTCCATTCTTTC 146  
QY 41 LeuLeuValIlyMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
DB 147 CTCCTGGTGAAATGAACACCCGGTCAGTGACCCACCATGGCGGTCTTAATTTGTGGTG 206

QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleIleValysThr 80  
DB 207 GTCACAGCGTCTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAGAGACT 266  
QY 81 TrpMetPheGlyLeuProPheCysValysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 267 TGGATGTTGGGCTGCCCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 326  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheCysCys 120  
DB 327 CTCACGTTCTATTCATGTTGGTATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 386  
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140  
DB 387 AAGACAAAGTGAATCTACAGAAATCGATGCTGTGCTGCCAGTCTGCGCATGTG 446  
QY 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
DB 447 ACCTGCTGATGTCATTGTTGTTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 506  
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIlyIle 180  
DB 507 TACATGAGGAGACCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGTGAAATC 566  
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
DB 567 ATCAACTATATGATAGTCATTTTGTATAGCCGTTGCTGTGATTTCTTGTGTTCTCCAG 626  
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DB 627 GTCTTCATCATATGTTGATGTTGTCAGAGACTACGCCACTCTTTACTATCCACACAGGAG 686  
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
DB 687 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTATCTCTTGTGTTTCTTCTTCCC 746  
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerHnAlaCysAsnSer 260  
DB 747 TACCAGTTCCTTAGGATCTTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 806  
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
DB 807 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTGTATGATTG 866  
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheGlyGlnIlyIleGlyLeuTrpAsn 300  
DB 867 CTCTCTCTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926  
QY 301 CysValLeuCysArg 305  
DB 927 TGTGTTTGTGCGGT 941  
RESULT 12  
AX646815 113306 bp DNA linear PAT 04-MAR-2003  
LOCUS Sequence 1007 from Patent EP1270724.  
DEFINITION AX646815  
ACCESSION AX646815  
VERSION AX646815.1 GI:28799225  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.  
TITLE Guanine triphosphate-binding protein coupled receptors  
AUTHORS Patent: EP 1270724-A 1007 02-JAN-2003;  
JOURNAL National Institute of Advanced Industrial Science and Technology  
(JP); Center for Advanced Science and Technology Incubation, Ltd.  
(JP)  
FEATURES  
Location/Qualifiers  
source 1. .113306

## ORIGIN

Alignment Scores:

[illegible]

U.S.-10-055-106C-2 (1-305) x AX709195 (1-1460)

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QY	21	IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe	40
Db	403	ATCAGGCTCTACTTCATAGTGTATTATGCGGGCTGGTGGGTGTCATTCCATCTTTTC	462
QY	41	LeuLeuValIlyMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal	60
Db	463	CTCCTGGTGAATAATGAACACCCGGTCAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGTG	522
QY	61	ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr	80
Db	523	GTCACAGCGTTTTCTGCTGACAGTGCATTTCCGTTGACTTACCTCATCAGAGAGACT	582
QY	81	TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr	100
Db	583	TGGATGTTTGGGCTGGCCTTCGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC	642
QY	101	LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys	120
Db	643	CTCACGTTCTATTCTATGTGTGATCCTGGTCCACGATACCTCATCTTCTTCAAGTGC	702
QY	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTrp	140
Db	703	AAAGACAAAGTGAATCTACAGAAAACCTGCATGCTGTGGCTGCAGTGTGGCATGTGG	762
QY	141	ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	763	ACGCTGGTGAATGTCAATTGTGGTACCCCTGGTGTCTCCCGGTATGAATCCATGAGAA	822
QY	161	TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle	180
Db	823	TACAAATCAGGAGCACGTGTTTAAATTCACAAAGAGCTTGCTTACACATATGTGAAATC	882
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln	200
Db	883	ATCAACTATATGATAGTCAATTTTGTCTAGCCGTTGCTGTGATTCGTGGTCTTCCAG	942
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220
Db	943	GTCTTCATCATATGATGTGGTGCAGAGCTACGCCACTCTTACTATCCACCAGAG	100
QY	221	PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro	240
Db	1003	TTCTGGGCTCAGCTGAAAACCTATTATTTTATAGGGGTCACTCTGTGTGTTCCTTCCC	1063
QY	241	TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer	260
Db	1063	TACAGTTCTTTAGGATCTATTACTTGAATGTGTGACGCATTCATGCTGTAAACAGC	1121
QY	261	LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu	280
Db	1123	AAGGTTGCATTTTATACGAAATCTCTCTTGAAGTGTAAACAGCAATTAGCTGTATGATTG	1181
QY	281	LeuLeuPheValPheGlySerHisTyrPheLysGlnLysIleIleGlyLeuTrpAsn	300
Db	1183	CTTCTCTTTCTTTGGGGAGCCATTGGTTTAGCAAAAGATTAATTGGGCTTATGAAT	1241
QY	301	CysValLeuCysArg	305

1243 TGTGTTTGTGCCGT 1257

## RESULT 10

AX147836	AX147836	Sequence 81 from Patent WO0136473.	2525 bp	DNA	linear	PAT 08-JUN-2001
LOCUS						
AX147836						
DEFINITION						
AX147836						
ACCESSION						
AX147836						
VERSION						
AX147836.1						
GI:14346839						

**KEYWORDS:** . Homo sapiens (human)  
**SOURCE:**

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

**AUTHORS**  
Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V., Seilitz, T. and Huff, R.M.

**TITLE** Novel g protein-coupled receptors  
**JOURNAL** Patent: WO 0136473-A 81 25-MAY-2001;

**JOURNAL**  
**FACE:** NO 0150473-A UT 25 MAR 2001  
**PHARMACIA & UPJOHN COMPANY (US)**  
**FEATURES**  
**Location/Qualifiers**

FEATURES  
SOURCE

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## ORIGIN

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Pred. No.:		Matches:	305
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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
PA:	5		

US-10-055-106C-2 (1-305) x AX147836 (1-2525)

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Qy	21	IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe	40
Db	87	ATCAGCCTTCACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCTTCCTTTTC	146
Qy	41	LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal	60
Db	147	CTCCTGGTGAATAATGAACACCCGGTCACTGACCACTGGCGGTCATTAACTTGGTGGT	206
Qy	61	ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr	80
Db	207	GTCACACCGCTTTTCGCTGACAGTGCCATTTCGCTTGACTACCTCATCAGAAGACT	266
Qy	81	TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr	100
Db	267	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCACTGTCACATCCACATGTAC	326
Qy	101	LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys	120
Db	327	CTCAGTTTCCTATTCTATGTGGTGATCTCTGGTCACCATACCTCATCTTCTTCAAGTGC	386
Qy	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTrp	140
Db	387	AAAGACAAAGTGGGAATTCACAGAAAACTGCATGCTGTGGCTGCCAGTGGCTGGCATGG	446
Qy	141	ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	447	ACGCTGGTGATTGTTCATTGTGGTACCCCTGGTTGCTCCCGGTATGGGAATCCATCAGGNA	506
Qy	161	TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle	180
Db	507	TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGCTTACACATATGTGAAATC	566



QY 241 TyrGlnPheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
 Db 939 TACCAGTTCCTTTAGGATCTATTACTTGAATGTGTGAGCGCATTCACATGCCCTGTAAACAGC 998  
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 Db 999 AAGGTGTGATTTTAAACGAAATCTTCTTGAGTGTACAGCAATTTAGCTGTATGATTTG 1058  
 QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleGlyLeuTrpAsn 300  
 Db 1059 CTTCTCTTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 1118  
 QY 301 CysValLeuCysArg 305  
 Db 1119 TGTGTTTGTGCCGT 1133  
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 AX709194 1340 bp DNA linear PAT 04-APR-2003  
 LOCUS AX709194  
 DEFINITION Sequence 53 from Patent WO02063004.  
 ACCESSION AX709194  
 VERSION AX709194.1 GI:29564788  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1  
 Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
 Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,  
 Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
 Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,  
 Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
 Harland, L.  
 G-protein coupled receptors  
 Patent: WO 02063004-A 53 15-AUG-2002;  
 Incyte Genomics, Inc. (US)  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
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 QY 1 MetProGlyHisAsnThrSerArgLysSerCysAspProIleValThrProHisLeu 20  
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 QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
 Db 283 ATCACCTCTACTTCTATAGTGTCTTATTTGGGGCTGTGGGTGCTATTCCTATCTTTTC 342  
 QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
 Db 343 CTCCTGGTGAATGAACACCCGGTCAGTGACCACCATGGCGGTCTATTAACCTTGGTGTG 402  
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80  
 Db 403 GTCCACAGCGTTTCTGCTGACGTGCGATTTCCCTTGACCTACTCTATCAGAGACT 462  
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100

Db 463 TGGATGTTGGGCTGCCCTTCTCCTCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 522  
 QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120  
 Db 523 CTCAGGTTCCTATTTCTATGTGGTGAATCCTGTGTCCAGATACCTCATCTTCTTCAAGTGC 582  
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaIleSerAlaGlyMetTrp 140  
 Db 583 AAGACAAAGTGAATTTCTACAGAAAGTGCATGTGTGGCTGCCAGTGTGCATGTGG 642  
 QY 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160  
 Db 643 AGCTGGTGTGATTCATTTGTGTACCCCTGGTGTCTCCGGTATGAATCCATGAGAA 702  
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
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 QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200  
 Db 763 ATCACTATATATGATGATCAATTTTGTATAGCGGTGTCTGTGATTTCTGTGTCTTCCAG 822  
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 Db 823 GTCTTCATCATATTGATGTGTGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 882  
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240  
 Db 883 TTTCTGGGCTCAGCTGAAGAAACCTATTTTATAGGGGTGATCTCTGTGTTGTTCTTCTTCCC 942  
 QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
 Db 943 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 1002  
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280  
 Db 1003 AAGTTGCAATTTTATACGAAATCTTCTTGAGTGTAAACAGCAAGATAATTGGCTTATGGAAT 1122  
 QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleGlyLeuTrpAsn 300  
 Db 1063 CTTCTCTTCTGCTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 1122  
 QY 301 CysValLeuCysArg 305  
 Db 1123 TGTGTTTGTGCCGT 1137  
 RESULT 9  
 AX709195 1460 bp DNA linear PAT 04-APR-2003  
 LOCUS AX709195  
 DEFINITION Sequence 54 from Patent WO02063004.  
 ACCESSION AX709195  
 VERSION AX709195.1 GI:29564789  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1  
 Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
 Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,  
 Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
 Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,  
 Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
 Harland, L.  
 G-protein coupled receptors  
 Patent: WO 02063004-A 54 15-AUG-2002;  
 Incyte Genomics, Inc. (US)  
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 /note="Incyte ID No: 90012670CB1"  
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 Alignment Scores:  
 Pred. No.: 1,47e-110 Length: 1460  
 Score: 1592.00 Matches: 305  
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 Best Local Similarity: 100.00% Mismatches: 0  
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Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuLeuLysThr 80
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Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisLysMetTyr 100
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Db 360 CTCACGTTCTCTATCTATGTTGGTGATGCTGCTGCACAGATACCTCATCTTCAAGTGC 419
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RESULT 7
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DEFINITION Sequence 52 from Patent WO02063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallick, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,
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Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,  
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
Harland, L.  
G-protein coupled receptors  
Patent: WO 02063004-A 52 15-AUG-2002;  
Incyte Genomics, Inc. (US)  
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Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 399 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 458
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University, Box 593, Uppsala 75124, Sweden

## FEATURES

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ACCESSION BD187510  
VERSION 1  
KEYWORDS JP 2003024082-A/1  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 918)  
AUTHORS Lee H.  
TITLE Novel Polypeptide  
JOURNAL Patent: JP 2003024082-A 1 28-JAN-2003;  
COMMENT Prizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)

OS Homo sapiens  
PN JP 2003024082-A/1  
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CC

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Pred. No.: 1.02e-110 Length: 918  
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Best Local Similarity: 100.00% Mismatches: 0  
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DEFINITION Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete cds.  
ACCESSION AY288420  
VERSION AY288420.1  
KEYWORDS GI:32165523  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 918)  
AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and Schioth,H.B.  
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives  
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)  
MEDLINE 22985413  
PubMed 14623098

2 (bases 1 to 918)  
AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E.I., Lagerstrom,M.C. and Schioth,H.B.  
TITLE Direct Submission  
JOURNAL Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala

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RESULT 3
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LOCUS Novel G protein-coupled receptor protein and its DNA.
DEFINITION
ACCESSION BD105324
VERSION BD105324.1 GI:22650898
KEYWORDS WO 0196567-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Moriya.T., Ito.T., Shintani,Y. and Miyajima,N.
Novel G protein-coupled receptor protein and its DNA
Patent: WO 0196567-A 1 20-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
PN WO 0196567-A/1
PD 20-DEC-2001
PF 14-JUN-2001 WO 2001JP005061
PR 15-JUN-2000 JP OOP 184596,19-JUL-2000 JP OOP 223887 PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00,

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ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Harland, L.  
TITLE Human g-protein coupled receptor  
JOURNAL Patent: EP 1225183-A 1 24-JUL-2002;  
Pfizer Limited (GB); PFIZER INC. (US)  
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ACCESSION AX498180  
VERSION AX498180.1 GI:23343111  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Chen, R., Chu, Z.L., Dang, H.T., Lowitz, K.P. and Pride, C.  
TITLE Endogenous and non-endogenous versions of human g protein-coupled receptors  
JOURNAL Patents: WO 0242461-A 3 30-MAY-2002;  
Arena Pharmaceuticals, Inc. (US)  
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GenCore version 5.1.6  
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Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

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Maximum Match 100%  
Listing first 45 summaries

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- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
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- 15: em.ba.\*
- 16: em.fun.\*
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- 19: em.mu.\*
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- 21: em.or.\*
- 22: em.ov.\*
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- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	1592	100.0	1336	6	AX709193 Sequence
8	1592	100.0	1340	6	AX709194 Sequence
9	1592	100.0	1460	6	AX709195 Sequence
10	1592	100.0	2525	6	AX147836 Sequence
11	1592	100.0	2525	6	AX521885 Sequence
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18	1293	81.2	167316	2	AC078995 Mus muscu
19	1176	73.9	972	6	AX657538 Sequence
20	1046	65.7	228766	2	AC099132 Rattus no
21	847	53.2	744	10	AY288432 Rattus no
22	787	49.4	456	9	AY255538 Homo sapi
23	750.5	47.1	140539	2	AC079758 Homo sapi
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27	588.5	37.6	188535	2	EX640462 Danio rer
28	547	34.4	393	10	AY255553 Mus muscu
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32	277	17.4	1146	5	AY241090 Gallus ga
33	252	15.8	1137	5	AY241119 Takifugu
34	249	15.6	137153	5	AL590151 Zebrafish
35	249	15.6	142350	5	EX088596 Zebrafish
36	248	15.6	1430	9	BC035750 Homo sapi
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ALIGNMENTS

RESULT 1

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Search completed: April 25, 2004, 18:51:08  
Job time : 2953 secs



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**ORGANISM**  
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**REFERENCE**  
**AUTHORS**  
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 GRASP Consortium, Davidson, W.S., Koop, B.F. and  
 http://web.uvic.ca/cbr/grasp.  
**TITLE**  
 A survey of Salmo salar transcripts from high complexity cDNA  
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**JOURNAL**  
**COMMENT**  
 Unpublished (2002)  
 Contact: Koop BF  
 Centre for Biomedical Research  
 University of Victoria  
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
 Tel: 250 472 4067  
 Fax: 250 472 4075  
 Email: bkoop@uvic.ca  
 Genome Sciences Centre, BC Cancer Agency  
 cDNA preparation, sequencing and bioinformatics:  
 Y Butterfield, R Kirkpatrick, J Asano, N Gira, R Guin, D Lee,  
 S Lee, T Olson, P Pandon, A Prabhu, D Smallus, L Spence, J Stott,  
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 Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),  
 Simon Jones (PNS, Nanaimo, B.C.), Seaspring Hatchery  
 (Crofton, B.C.), Rachel Roper (University of Victoria)"

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 Stegomyia.  
**REFERENCE**  
 1 (bases 1 to 501)  
 Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
**AUTHORS**  
 End sequencing of Aedes aegypti BACs  
**TITLE**  
 Unpublished (2003)  
**JOURNAL**  
**COMMENT**  
 Other GSSs: CSU-K34.117019.T7  
 Contact: Brendan Loftus  
 Department of Eukaryotic Genomics  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-3543  
 Fax: 301-838-0208  
 Email: ente@tigr.org  
 Library was provided by Susan Brown and Dennis Knudson at Colorado

State University.  
 Seq primer: SP6  
 Class: BAC ends.  
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 Reference: SINGH, K. R. P. 1967 Cell cultures derived  
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 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
**AUTHORS**  
 Direct Submission  
**TITLE**  
**JOURNAL**  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
**COMMENT**  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nh@sanger.ac.uk  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.  
**FEATURES**  
 source  
 1..338  
 Location/Qualifiers  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="372G04"

**ORIGIN**  
 Query Match 2.3%; Score 21; DB 29; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
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/clone="IMAGE:3988230"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI-CCAP_Lu29"
/note="Organ: lung; Vector: pCMV-Sport6; Site: 1; SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match          2.8%; Score 27; DB 10; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCTTCTGCAAAATTTGTGAGTGCATG 282
      |||||
Db 165 CCCTTCTGCAAAATTTGTGAGTGCATG 191

RESULT 9
AZ554824
LOCUS
DEFINITION
  RPCI-23-211E13-TV RPCI-23 DNA linear GSS 20-NOV-2000
ACCESSION
  RPCI-23-211E13, genomic survey sequence.
VERSION
  AZ554824.1 GI:11234644
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
  1 (bases 1 to 580)
  Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
  Akinret, B., Levins, M., McGann, S., Teegaye, G., Geer, K., Krol, M., de
  Jong, P., and Fraser, C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other GSSs: RPCI-23-211E13.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@igir.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (http://www.reschgen.com). BAC end page:
  http://www.tigr.org/tdb/bacends/mouse/bac\_end\_intro.html
  Plate: 211 row: E column: 13
  Seq primer: T7
  Class: BAC ends.

FEATURES
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        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="RPCI-23-211E13"
        /sex="Female"
        /lab_host="DH10B"
        /clone_lib="RPCI-23"
        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
        EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney_and/or
        brain genomic DNA was isolated and partially digested
        with a combination of EcoRI and EcoRI MethyIase. Size

```

```

selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "

ORIGIN
Query Match          2.8%; Score 26; DB 28; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 TTACTATCCACCAGGAGTTCTGGC 668
      |||||
Db 257 TTACTATCCACCAGGAGTTCTGGC 282

RESULT 10
CB514250/c
LOCUS
DEFINITION
  ssalr5b548309 mixed_tissue Salmo salar cDNA, mRNA linear EST 16-MAY-2003
ACCESSION
  CB514250
VERSION
  CB514250.1 GI:29325476
KEYWORDS
  EST.
SOURCE
  Salmo salar (Atlantic salmon)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
  Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
  1 (bases 1 to 648)
  GRASP Consortium, Davidson, W.S., Koop, B.F. and
  http://web.uvic.ca/cbr/grasp.
  A survey of Salmo salar transcripts from high complexity cDNA
  libraries
  Unpublished (2002)
  Contact: Koop BF
  Centre for Biomedical Research
  University of Victoria
  PO Box 3020, STN CSC, Victoria BC, V8W 3N5, Canada
  Tel: 250 472 4067
  Fax: 250 472 4075
  Email: bkoop@vic.ca
  Genome Sciences Centre, BC Cancer Agency cDNA preparation,
  sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
  Asano, N Ginn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D
  Smalius, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and
  M Marra.

FEATURES
  source
    1..648
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        /organism="Salmo salar"
        /mol_type="mRNA"
        /strain="McConnell"
        /db_xref="taxon:8030"
        /clone_lib="mixed tissue"
        /note="Vector: pCMVSPORT6; Library Creator: Research
        Genetics; Atlantic salmon tissue contributors: Carlo
        Blagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
        Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
        (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN
Query Match          2.8%; Score 26; DB 14; Length 648;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 CACCAGGAGTTCTGGGCTCAGCTGAA 677
      |||||
Db 496 CACCAGGAGTTCTGGGCTCAGCTGAA 471

RESULT 11
CA050323/c
LOCUS
DEFINITION
  ssalr5b520231 mixed_tissue Salmo salar cDNA, mRNA linear EST 04-MAR-2003
ACCESSION
  CA050323
VERSION
  CA050323.1 GI:24380566

```

```

Best Local Similarity 100.0%; Pred. No. 1.1e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 42; Conservative 0;

QY 38 ATCTATAGTACACCCCACTTAATCAGCTCTACTTCATAG 79
Db 143 ATCTATAGTACACCCCACTTAATCAGCTCTACTTCATAG 184

RESULT 6
AQ425698/c
LOCUS
DEFINITION
  AQ425698 575 bp DNA linear GSS 24-MAR-1999
  CITBI-E1-2569B12.TF CITBI-E1 Homo sapiens genomic clone 2569B12,
  genomic survey sequence.
ACCESSION
  AQ425698
VERSION
  AQ425698.1 GI:4495786
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 575)
AUTHORS
  Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
  Venter,J.C.
TITLE
  Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
  Map Building
JOURNAL
  Unpublished (1997)
COMMENT
  Other GSSs: CITBI-E1-2569B12.TR
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbest@igf.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
  Seq primer: MJ3-21
  Class: BAC ends.
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    1..575
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    /mol_type="genomic DNA"
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    /clone="2569B12"
    /sex="male"
    /cell_type="sperm"
    /clone_lib="CITBI-E1"
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    CalTech Human BAC Library D"

ORIGIN
Query Match 3.2%; Score 29; DB 28; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGTCGCCACATACCTCCAGGAATTC 29
Db 30 ATGCGTCGCCACATACCTCCAGGAATTC 2

RESULT 7.
BG862323
LOCUS
DEFINITION
  BG862323 646 bp mRNA linear EST 29-MAY-2001
  602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
  mRNA sequence.
ACCESSION
  BG862323
VERSION
  BG862323.1 GI:14212861
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
  1 (bases 1 to 772)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
  Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM9196 row: f column: 07
  High quality sequence stop: 634.
  Location/Qualifiers
    1..772
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    /clone="IMAGE:4917024"
    /tissue_type="tumor, gross tissue"
    /dev_stage="5 months"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP Mam4"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
    Library constructed by Life Technologies. Investigators
    providing samples: Lothar Hennighausen/Priscilla Furth,
    NIH Reference for transgenic model: Li et al., Cell Growth
    and Differentiation 7, 3-11 (1996)."
```

```

REFERENCE
  1 (bases 1 to 646)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
  Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM10828 row: b column: 01
  High quality sequence stop: 644.
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    1..646
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    /strain="NMRI"
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    /clone="IMAGE:4917024"
    /tissue_type="tumor, gross tissue"
    /dev_stage="5 months"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP Mam4"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
    Library constructed by Life Technologies. Investigators
    providing samples: Lothar Hennighausen/Priscilla Furth,
    NIH Reference for transgenic model: Li et al., Cell Growth
    and Differentiation 7, 3-11 (1996)."
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## ORIGIN

```

Query Match 2.9%; Score 27; DB 12; Length 646;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCTTCGCAAAATTTGTGAGTGCCATG 282
Db 562 CCCTTCGCAAAATTTGTGAGTGCCATG 588

RESULT 8
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LOCUS
DEFINITION
  BF160725 772 bp mRNA linear EST 30-OCT-2000
  601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',
  mRNA sequence.
ACCESSION
  BF160725
VERSION
  BF160725.1 GI:11040832
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 772)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Gilbert Smith, Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM9196 row: f column: 07
  High quality sequence stop: 634.
  Location/Qualifiers
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    /strain="NMRI"
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    /clone="IMAGE:4917024"
    /tissue_type="tumor, gross tissue"
    /dev_stage="5 months"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP Mam4"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
    Library constructed by Life Technologies. Investigators
    providing samples: Lothar Hennighausen/Priscilla Furth,
    NIH Reference for transgenic model: Li et al., Cell Growth
    and Differentiation 7, 3-11 (1996)."
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## FEATURES

source

TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL	Unpublished (2003)
COMMENT	Contact: YiXin Zeng

```

FEATURES
source
Email: yxzeng@grsums.edu.cn.
Location/Qualifiers
1..499
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

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Query Match	20.6%	Score 189;	DB 14;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 28-89;		
Matches 189;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

1	ATGCCTGGCCCAATPACCTCAGAGAAATCCCTCTTGGCATCCTATAGTGACACCCCACTTA	60
311	ATGCCTGGCCCAATPACCTCAGAGAAATCCCTCTTGGCATCCTATAGTGACACCCCACTTA	370
61	ATCAGCCTCTACTTCATATAGTCTTATTGGGGGGCTGGTGGTGTCAATTCATCTTTTC	120
371	ATCAGCCTCTACTTCATATAGTCTTATTGGGGGGCTGGTGGTGTCAATTCATCTTTTC	430
121	CTCCTGTGTGAAAAATGAACACCCGGTTCAGTGACACCAACATGGCGGTCTAATTAACATTGGTGGTG	180
431	CTCCTGTGTGAAAAATGAACACCCGGTTCAGTGACACCAACATGGCGGTCTAATTAATTTGGTGGTG	490

[illegible]

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FEATURES
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/mol_type="mRNA"  
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/clone\_lib="Achromys KRC Library"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

## ORIGIN

	Query Match	16.1%;	Score 148;	DB 12;	Length 283;
	Best Local Similarity	100.0%;	Pred. No. 1.6e-67;		
	Matches 148;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA	60		
Db	136	ATGCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA	195		
QY	61	ATCAGCGCTCTACTTTCATAGTGCTTATTGGCGGCGCTGGTGGGTGCTCATTTCCATTCTTTTC	120		
Db	196	ATCAGCGCTCTACTTTCATAGTGCTTATTGGCGGCGCTGGTGGGTGCTCATTTCCATTCTTTTC	255		
QY	121	CTCCTGGTGAATAATGAACACCCGGTCAG	148		
Db	256	CTCCTGGTGAATAATGAACACCCGGTCAG	283		

LOCUS	649 bp	mRNA	linear	EST 21-APR-2001
RG461295	RG461295	Athersys RAGE Library Homo sapiens	cDNA, mRNA	sequence.
DEFINITION	EST404080			
ACCESSION	RG461295			
VERSION	RG461295.1	GI:13749801		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

FEATURES  
SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/call_line="Hr1080"
/clone_lib="Athersys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is Hr1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in Hr1080 under normal circumstances."

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ORIGIN

Query Match 4.6%; Score 42; DB 12; Length 649;

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/call_line="Htt080"
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/notes="See 'Creation of Genome-Wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though
cell type identified is Htt080, since a random activation
method was used, these sequence tags are not necessarily
expressed in Htt080 under normal circumstances."

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```

/call_line="H1080"
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/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is H1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in H1080 under normal circumstances."

```

end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6  
R.site 1 : EcoRI  
R.site 2 : EcoRI  
Location/Qualifiers  
1. .684  
/organism="Pan troglodytes"  
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/db\_xref="taxon:9598"  
/clone="RP43-007G22.TJ"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RPCI-43 Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 50.4%; Score 463; DB 29; Length 684;  
Best Local Similarity 99.8%; Pred. No. 3.8e-236;  
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
376 TTCTACAGAAACTGATGCTGGCTGCCAGTGTGGCATGTGGACGTGGTGTGATGTC 435  
Db 25 TTCTACAGAAACTGATGCTGGCTGCCAGTGTGGCATGTGGACGTGGTGTGATGTC 84  
QY 436 ATTGTGGTACCCCTGTTGTTCTCCCGTATGGAATCCATCAGGATACAAATCAGAGCAC 495  
Db 85 ATTGTGGTACCCCTGTTGTTCTCCCGTATGGAATCCATCAGGATACAAATCAGAGCAC 144  
QY 496 TGTGTTTAAATTCACAAAGAGCTGTGTACACATATGTGAAATCATCACTATATGATA 555  
Db 145 TGTGTTTAAATTCACAAAGAGCTGTGTACACATATGTGAAATCATCACTATATGATA 204  
QY 556 GTCATTTTGTATACCGTGTGTGATGCTGTTGGCTTCCAGTCTTCATCAATATG 615  
Db 205 GTCATTTTGTATACCGTGTGTGATGCTGTTGGCTTCCAGTCTTCATCAATATG 264  
QY 616 TTGATGGTCAGAGCTAGCCACTCTTTACTATCCACAGAGTTCGGCTCAGCTG 675  
Db 265 TTGATGGTCAGAGCTAGCCACTCTTTACTATCCACAGAGTTCGGCTCAGCTG 324  
QY 676 AAAAACTATTTTATAGGGTCACTCTTGTGTTTCTTCTCCCTACAGTCTTTAGG 735  
Db 325 AAAAACTATTTTATAGGGTCACTCTTGTGTTTCTTCTCCCTACAGTCTTTAGG 384  
QY 736 ATCTATTACTGATCTGTGACGATTCGATCCCTGTAACAGCAAGTTCGATTTAT 795  
Db 385 ATCTATTACTGATCTGTGACGATTCGATCCCTGTAACAGCAAGTTCGATTTAT 444  
QY 796 AACGAAATCTTCTTGATGTAACAGCAATTAGCTGTATGTTGCTTCTCTTTGCTTT 855  
Db 445 AACGAAATCTTCTTGATGTAACAGCAATTAGCTGTATGTTGCTTCTCTTTGCTTT 504  
QY 856 GGGGGAAGCCATTGTTTAAAGCAAGATAATTG 889  
Db 505 GGGGGAAGCCATTGTTTAAAGCAAGATAATTG 538

RESULT 2

AQ888495

LOCUS

DEFINITION

HS\_3162\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

1 (bases 1 to 456)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
99380589  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 3162 row: D column: 1  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 456.

FEATURES

source

1. .456  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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Db 61 GTGTGATCCCTGGTGTGTTCTCCGATGGAATCCATCAGGAATACATAGGAGCACTGT 120  
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RESULT 3

CD699779

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

AUTHORS

Zeng,Y.-X.

CD699779 499 bp mRNA linear EST 25-JUN-2003  
EST161303 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
CD699779  
CD699779.1 GI:32229387  
EST.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: April 25, 2004, 16:55:20 ; Search time 2948 Seconds  
(without alignments)  
9299.010 Million cell updates/sec

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  - 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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REFERENCE  
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JOURNAL  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

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Pan troglodytes  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
Fujiyama, A., Hattori, M., Toyoda, A., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library RPCI-43  
Unpublished  
2 (bases 1 to 684)  
Fujiyama, A., Hattori, M., Toyoda, A., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suhei-ro-chou, Tsukuba, Ibaraki, Japan 305-8565, Japan  
(E-mail: chimpanzee@gsic.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/)  
Tel: 81-45-503-9111, Fax: 81-45-503-9170  
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

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Job time : 3931 secs



REFERENCE  
AUTHORS Deleersnijder W., Blockx, H. and de Moor, I.  
TITLE Human g-protein coupled receptor and uses thereof  
JOURNAL Patent: WO 0244212-A 1 06-JUN-2002;  
SOLWAY PHARMACEUTICALS B V (NL)  
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ACI46385.2 GI:38154073  
HTG, HTGS PHASE1  
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SOURCE  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE The sequence of Pan troglodytes clone  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Unpublished  
COMMENT  
Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 164055)  
Wilson, R.K.  
Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
On Nov 4, 2003 this sequence version replaced gi:33620890.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: C\_PT126C06  
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Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; Version 0.990319  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 AUTHORS  
 Baughn, M.R., Graul, R.C., Wallia, N.K., Gandhi, A.R., Hafalia, A.J.,  
 Rankumar, J., Tribouley, C.M., Thornton, M., Kallick, D.A., Yao, M.G.,  
 Elliott, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,  
 Roopa, R., Nguyen, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and  
 Policky, J.L.  
 G-protein coupled receptors  
 Patent: WO 0226825-A 22 04-APR-2002;  
 Incyte Genomics, Inc. (US)  
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 JOURNAL  
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RESULT 14

AX453412

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

AX453412

Sequence 1 from Patent WO20244212.

AX453412.1

GI:21712725

Homo sapiens (human)

1051 bp

DNA

linear

PAT 06-JUL-2002

RESULT 14					
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DEFINITION	AX53412				
ACCESSION	AX53412				
VERSION	AX53412.1	GI:21712725			
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ORGANISM	Homo sapiens				

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 ACCESSION  
 VERSION GI:24410791  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Lind, P., Parodi, L.A., Vogeli, G. and Wood, L.S.  
 G protein-coupled receptor  
 Patent: WO 02064789-A 81 22-AUG-2002;  
 JOURNAL PHARMACIA & UPJOHN COMPANY (US)  
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ACCESSION AX147836  
VERSION AX147836.1 GI:14346839  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Vogeli, G., Wood, L. S., Parodi, L. A., Hiebsch, R. R., Lind, P.,  
Slightom, J., Schellin, K. A., Kaytes, P. S., Bannigan, C. M., Ruff, V.,

Sejltz, T. and Huff, R. M.  
Novel g protein-coupled receptors  
Patent: WO 0136473-A 81 25-JUN-2001;  
PHARMACIA & UPJOHN COMPANY (US)  
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VERSION AX709194.1 GI:29564788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallick,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 53 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
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VERSION AX709195.1 GI:29564789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallick,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 54 15-AUG-2002;
Incyte Genomics, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGGGATCCTATAGTGACCCCACTTA 60
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LOCUS AX709193 1336 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 52 from Patent WO02063004.  
ACCESSION AX709193  
VERSION AX709193.1 GI:29564787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,  
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,  
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,  
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,

Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and  
Harland, L.  
G-protein coupled receptors  
Patent: WO 02063004-A 52 15-AUG-2002;  
Incyte Genomics, Inc. (US)  
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QY 61 ATCAGCCTCTACTTCTATAGTCTTATTTGGGGGCTGTGGGTGTCATTTCCATTCTTTC 120  
DB 279 ATCAGCCTCTACTTCTATAGTCTTATTTGGGGGCTGTGGGTGTCATTTCCATTCTTTC 338  
QY 121 CTCCTGGTGAAGTGAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATCTGGTGGT 180  
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QY 181 GTCACAGCGTTTCTGCTGACAGTGCCTATTTGGTGGTACCTACCTCATCAAGAGACT 240  
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DB 639 ACGTGGTGAATGTCATGTTGTGACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 698  
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TITLE		Novel Polypeptide		Patent: JP 2003024082-A 1 28-JAN-2003;		Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)	
JOURNAL		OS Homo sapiens		PN JP 2003024082-A/1		PD 28-JAN-2003	
COMMENT		PR 17-JAN-2002 JP 2002008881		PF 23-JAN-2001 GB 0101739.1		PI harland lee	
PI		CC		FH		Key	
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Db	1	ATGCTGGCCACAATACCTCCAGGAATTCCTTTGGATCCTATAGTGACACCCCACTTA	60	Qy	61	ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGGTGGTGGTGCATTCCTATCTTTTC	120
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Db	241	TGGATGTTTGGCTGCGCTTCTGCAAAATTTGTAGTGCCATGCTGCATCCACATGTAC	300	Qy	301	CTCAGTTCCCTATCTATGTTGGTGTCTGTCACAGATACCTCACTCTTCAAGTGC	360
Qy	301	CTCAGTTCCCTATCTATGTTGGTGTCTGTCACAGATACCTCACTCTTCAAGTGC	360	Db	301	CTCAGTTCCCTATCTATGTTGGTGTCTGTCACAGATACCTCACTCTTCAAGTGC	360
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Db	901	TGTGTTTGTGCGGTAG	918
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DEFINITION	Novel G protein-coupled receptor protein and its DNA.		
ACCESSION	BD105324		
VERSION	BD105324.1	GI:22650898	
KEYWORDS	WO 0196567-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Moriya.T., Ito.T., Shintani.Y. and Miyajima.N.		
JOURNAL	Novel G protein-coupled receptor protein and its DNA		
COMMENT	Patent: WO 0196567-A 1 20-DEC-2001;		
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	PN WO 0196567-A/1		
	PD 20-DEC-2001		
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	A61K38/00,		
	PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC		
	A61P29/00,		
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DEFINITION	Novel Polypeptide.		
ACCESSION	BD187510		
VERSION	BD187510.1	GI:32997249	
KEYWORDS	JP 2003024082-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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FEATURES Pfizer Limited (GB) ; PFIZER INC. (US)  
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Best Local Similarity 100.0%; Pred. No. 0;  
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LOCUS  
DEFINITION  
Sequence 3 from Patent WO0242461.  
ACCESSION  
AX498180  
VERSION  
AX498180.1 GI:23343111  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.  
Endogenous and non-endogenous versions of human g protein-coupled  
receptors  
Patent: WO 0242461-A 3 30-MAY-2002;  
Arena Pharmaceuticals, Inc. (US)  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 17:44:40 ; Search time 3928 Seconds  
(without alignments)  
10129.558 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgcctggccacaataacac.....attgtgtttgtgcgcgttag 918

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 12

Total number of hits satisfying chosen parameters: 588639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_ov.\*

22: em\_or.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rtd.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	918	100.0	918	6	AX481576	AX481576 Sequence
2	918	100.0	918	6	AX498180	AX498180 Sequence
3	918	100.0	918	6	BD105324	BD105324 Novel G p
4	918	100.0	918	6	BD187510	BD187510 Novel Pol
5	918	100.0	918	9	AX288420	AX288420 Homo sapi
6	918	100.0	1336	6	AX709193	AX709193 Sequence
7	918	100.0	1340	6	AX709194	AX709194 Sequence
8	918	100.0	1460	6	AX709195	AX709195 Sequence
9	918	100.0	2525	6	AX147836	AX147836 Sequence
10	918	100.0	2525	6	AX521885	AX521885 Sequence
11	918	100.0	113306	6	AX646815	AX646815 Sequence
12	918	100.0	218186	9	AC083865	AC083865 Homo sapi
13	887	96.6	1499	6	AX451925	AX451925 Sequence
14	867	94.4	1051	6	AX453412	AX453412 Sequence
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16	690	75.2	972	6	AX57538	AX57538 Sequence
17	456	49.7	456	9	AY255538	AY255538 Homo sapi
18	436	47.5	140539	2	AC079758	AC079758 Homo sapi
19	306	33.3	447	6	AX147776	AX147776 Sequence
20	306	33.3	447	6	AX521825	AX521825 Sequence
21	39	4.2	39	6	AX453425	AX453425 Sequence
22	31	3.4	744	10	AY288432	AY288432 Rattus no
23	31	3.4	228766	2	AC099132	AC099132 Rattus no
24	29	3.2	29	6	AX498203	AX498203 Sequence
25	28	3.1	28	6	AX498202	AX498202 Sequence
26	27	2.9	918	10	AY288427	AY288427 Mus muscu
27	27	2.9	167316	2	AC078995	AC078995 Mus muscu
28	27	2.9	206999	10	AC122886	AC122886 Mus muscu
29	26	2.8	26	6	AX498231	AX498231 Sequence
30	26	2.8	26	6	BD105329	BD105329 Novel G p
31	26	2.8	393	10	AY255553	AY255553 Mus muscu
32	24	2.6	24	6	AX147890	AX147890 Sequence
33	24	2.6	24	6	AX147919	AX147919 Sequence
34	24	2.6	24	6	AX521939	AX521939 Sequence
35	24	2.6	24	6	AX521968	AX521968 Sequence
36	24	2.6	24	6	BD105326	BD105326 Novel G p
37	24	2.6	26	6	AX498200	AX498200 Sequence
38	24	2.6	52	6	AX147891	AX147891 Sequence
39	24	2.6	52	6	AX147920	AX147920 Sequence
40	24	2.6	52	6	AX521940	AX521940 Sequence
41	24	2.6	52	6	AX521969	AX521969 Sequence
42	23	2.5	23	6	AX147892	AX147892 Sequence
43	23	2.5	23	6	AX147921	AX147921 Sequence
44	23	2.5	23	6	AX521941	AX521941 Sequence
45	23	2.5	23	6	AX521970	AX521970 Sequence

#### ALIGNMENTS

RESULT 1  
AX481576  
LOCUS  
DEFINITION  
Sequence 1 from Patent EP1225183.  
AX481576  
ACCESSION  
VERSION  
AX481576.1 GI:22316490  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1  
AUTHORS  
Harland, L.  
TITLE  
Human g-protein coupled receptor  
JOURNAL  
Patent: EP 1225183-A 1 24-JUL-2002;

Mon Apr 26 12:47:10 2004

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; Patent No. 5046026
; GENERAL INFORMATION:
; APPLICANT: EPLER, CECIL
; APPLICANT: OZENERGER, BRADLEY
; APPLICANT: HUMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A81RUS1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Rat
; US-08-676-351-1

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Query Match      6.5%; Score 59.8; DB 3; Length 2706;
Best Local Similarity 45.6%; Pred. No. 9e-08;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

QY 65 GCCTCTACTTCAATAGTCTTATTGGCGGCTGGTGGG---TGTCATTTCCATCTTTTCC 121
Db 264 GGCTCTACTTGGCTGTGTGCTATCGGGGGCTCTCTGGGAACCTGCTCATGTATGTCA 323

QY 122 TCCTGTGTGAATGACACCCGCTCAGTCACACCATGCGGTCACTTAACCTTGGTGGTGG 181
Db 324 TCCTAGGCACACCAAGATGAGACAGCTACCAACATTTACATNTTATCTGGCACATGG 383

QY 182 TCCACAGCGTTTTTCTGTGTCAGAGTGCCTATTTGCTTGACCTACCTCATCAAGAAGACTT 241
Db 384 CTGATACCCCTGGTCTTGTGTAACACTGCCCTTCAGGGCACAGACATCCTACTGGGCTTCT 443

QY 242 GGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTACC 301
Db 444 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTTGTGCTATCGACTACTACAACTGTTTA 503

QY 302 TCACGTTTCCTATTTCTATGTGGTGATCCTGTGTCACAGATACCTCATCTTTCTTCAAGTCA 361
Db 504 CCAGCACTTTTACTCTGACCGCATGACGCTAGACGCTATGTGGCTATCTGCCACCTTA 563

QY 362 AAGACAAAGTGGAAATCTACAGAAACTGCTGTGCTGCGCATGCTGCGCATGTGGA 421
Db 564 TCCGTGCCCTTGATGTTCGGACATCCAGCAAAAGCCAGGCTGTAAATGTGGCCATATGGG 623

QY 422 CGCTGTGTGATTTGTCATTGTGTGTTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGAAT 481
Db 624 CCTGCTTCAGTGGTGGTGTCTCTGTTGCCATCATGGGTCAGCAAGTGGAGATG 583

QY 482 ACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTCTTACATATGTGAAATCA 541
Db 684 AAGAGATCGAGTGCCTGTGGAGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATTGG 743

QY 542 TCAACTATATGATGATGATTTTGTATAGCCGCTGCTGTGATTTCTGTTGGTCTTCCAGG 601
Db 744 CCATCTGCACTCTCTTTTCTCTCTATCATCCCTGTGTGATCATCTCTGTCTGTCTACA 803

QY 602 TCTTCATCATTT 612
Db 804 GCCTCATGATT 814

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Search completed: April 25, 2004, 17:46:11  
Job time: 93 secs

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 ORIGINAL SOURCE:  
 TISSUE TYPE: Rat brain  
 US-08-454-549-1

Query Match 6.5%; Score 59.8; DB 2; Length 2706;  
 Best Local Similarity 45.6%; Pred. No. 9e-08;  
 Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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Qy 65 GCCTCTACTTCCATAGTCTTATTGGGGGCTGGTGGG---TGTCAATTCATTTCTTTCC 121
Db 264 GGCTCTACTTGGCTGTGTCATCGGGGGGCTCTGGGGAACCTGCTCGTCATGTATGCA 323

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Db 324 TCCTCAGGACACCAAGATGAAGACAGCTACCAACATTTACATATTAACTGGCACTGG 383

Qy 182 TCCACAGCGTTTTCGTGACAGTCCGCTGAGTACACCATGGGTCATTAACTTGGTGGTGG 241
Db 384 CTGATACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443

Qy 242 GGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTACC 301
Db 444 GGCCATTGGGAATGCACTCTGCAAGACTGTCATTTCTATCGACTACTACAAATGTTA 503

Qy 302 TCACGTTCTCTATTCTGATGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 504 CCAGCAGCTTTTACTCTGACCCGCTGAGCTGAGACCGCTATGTGGCTATCTGCCACCTA 563

Qy 362 AAGACAAGTGAATTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
Db 564 TCCGTGCCCTTGTGATGCTGCAATTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 623

Qy 422 CGCTGGTGAATTTCTGCAATTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 481
Db 624 CCCTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683

Qy 482 ACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCA 541
Db 684 AAGAGATCGAGTGGCTGGTGGGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATTGG 743

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Db 744 CCATCTGATCTTCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 803

Qy 602 TCTTCATCAT 612
Db 804 GCCTCATGATT 814

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## RESULT 14

US-08-454-552-1  
 ; Sequence 1, Application US/08454552  
 ; Patent No. 6005072

## GENERAL INFORMATION:

APPLICANT: EPPLER, C. Mark  
 APPLICANT: OZENERGER, Bradley A.  
 APPLICANT: HUMES, Jeffrey D.  
 TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED  
 TO OPIOID RECEPTORS  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, P.C.  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/454,552  
 FILING DATE: 30-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Robinson, Joseph R.  
 REGISTRATION NUMBER: 33,448  
 REFERENCE/DOCKET NUMBER: 0646/1A818-US4  
 TELEPHONE: (212) 527-7700  
 TELEFAX: (212) 753-6237  
 TELEX: 236687  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2706 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 ORIGINAL SOURCE:  
 TISSUE TYPE: Rat brain  
 US-08-454-552-1

Query Match 6.5%; Score 59.8; DB 3; Length 2706;

Best Local Similarity 45.6%; Pred. No. 9e-08;  
 Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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Qy 65 GCCTCTACTTCCATAGTCTTATTGGGGGCTGGTGGG---TGTCAATTCATTTCTTTCC 121
Db 264 GGCTCTACTTGGCTGTGTCATCGGGGGGCTCTGGGGAACCTGCTCGTCATGTATGCA 323

Qy 122 TCCTGGTGAATGAACACCCGGTCAAGTACACACCATGGGTCATTAACTTGGTGGTGG 181
Db 324 TCCTCAGGACACCAAGATGAAGACAGCTACCAACATTTACATATTAACTGGCACTGG 383

Qy 182 TCCACAGCGTTTTCGTGACAGTCCGCTGAGTACACCATGGGTCATTAACTTGGTGGTGG 241
Db 384 CTGATACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443

Qy 242 GGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 301
Db 444 GGCCATTGGGAATGCACTCTGCAAGACTGTCATTTCTATCGACTACTACAAATGTTA 503

Qy 302 TCACGTTCTCTATTCTGATGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 504 CCAGCAGCTTTTACTCTGACCCGCTGAGCTGAGACCGCTATGTGGCTATCTGCCACCTA 563

Qy 362 AAGACAAGTGAATTTCTGCAATTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 421
Db 564 TCCGTGCCCTTGTGATGCTGCAATTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 623

Qy 422 CGCTGGTGAATTTCTGCAATTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 481
Db 624 CCCTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683

Qy 482 ACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCA 541
Db 684 AAGAGATCGAGTGGCTGGTGGGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATTGG 743

Qy 542 TCAATATATGATGATCATTTTGTGATAGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTG 601
Db 744 CCATCTGATCTTCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 803

Qy 602 TCTTCATCAT 612
Db 804 GCCTCATGATT 814

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## RESULT 15

US-08-676-351-1  
 ; Sequence 1, Application US/08676351C

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QY 182 TCACAGCGTTTCTCTGACAGTGCCATTTCGCTTGACCTACCTCATCAAGAGACTT 241
Db 450 CTGATACCCCTGGTCTTCTAACAACCTGCCCCCTCCAGGGCAGACATCCTACTGGGCTTCT 509
QY 242 GGATGTTTGGGCTGCCCTTCTGCAAAATTGTGAGTGCCATGCTGCACATCCACATGTACC 301
Db 510 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTATGCTATCGACTACTACAACATGTTTA 569
QY 302 TCAGTTCCTATTCTATGTGGTGATCCTGCTGCCAGATACCTTCCTTCTCAAGTGA 361
Db 570 CCAGCACTTTTACTCTGACCGCCAGAGCGTAGACCGCTATGTGGCTATCTGCCACCTTA 629
QY 362 AAGACAAAGTGAATTTCTACAGAAAACCTGATGCTGGTGGCCAGTGTGGCATGTGA 421
Db 630 TCCGTGCCCTTGATGTTGCGGACATCCAGCAAGCCAGGCTGTTAATGTGGCCATATGG 689
QY 422 GCGTGGTGATGTCATTGTGGTACCCCTGCTGCTCCCGTATGGAATCCATGAGGAAT 481
Db 690 CCGTGGCTTCACTGCTGGTGGTCTTCTGTCGCAATCATGGGTTGAGCAAGTGAAGATG 749
QY 482 ACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATCA 541
Db 750 AAGAGATCGAGTGCTGCTGGTGGAGATCCCTGCCCTCAGGACTATGGGGCCCTGTATCG 809
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Db 810 CCATCTGCATCTTCCCTTTTCTTCATCATCCCTGCTGCTGATCATCTCTGTCTGTACTA 869
QY 602 TCTTCATCAT 612
Db 870 GCCTCATGAT 880

RESULT 12
US-08-986-209A-1
; Sequence 1, Application US/08986209A
; Patent No. 6660496
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Pasternak, Gavril W
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTORS
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 830002-2004
; CURRENT APPLICATION NUMBER: US/08/986.209A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1402)
; OTHER INFORMATION:
US-08-986-209A-1

Query March 6.5k; Score 59.8; DB 4; Length 2600;
Best Local Similarity 44.8k; Pred. No. 8.8e-08;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

QY 9 CCACAATACCTCCAGGAATTCCTTTGGATCCTTATAGTGACACCCCACTTAATCAGCCT 68
Db 400 CCTCAATGCTAGCCACAGTGCCTTCTGCCCTTGGACTCAAGTCCACCATCGTGGGGCT 459
QY 69 CTACTTCATAGTCTTATTGGGGGCTGGTGG--TGTCATTTCCATTTCTTCTCCCT 125
Db 460 CTACTTGGCTGTGTCATCGGGGGCTCTCTGGGAAGTCCCTCTGTCATGTATGTCATCCT 519
QY 126 GGTGAAATGAACACCCGGTCAAGTACCAACCATGCGGTCAATTAACCTGGTGGTCA 185
Db 520 CAGGCACACCAAGATGAAGACTGTGTACCAACATTTACATATTTAATCTGGCACTGGCTGA 579
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QY 186 CAGCGTTTTTCTGTCAGAGTGCCATTTCGCTTGACCTACCTCATCAAGAGACTTGGAT 245
Db 580 TACCTCGTCTTCTGTCAGACTGCCCTTCCAGGGCAGACATCCTCTCTGGGCTTCTGGCC 639
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Db 640 ATTTGGGAATGCACTGTGCAAGCGGTCAATTTGCTATCGACTACTACAACATGTTTACCAG 699
QY 306 GTTCTATTCTATGTGGTGATCCTGTCACCCAGATACCTCATCTTCTCAAGTGCNAAGA 365
Db 700 CACTTTCATTTGACTGCCATGAGTAGACCGTTATGTAGTATCTGCCCACCTATCCG 759
QY 366 CAAAGTGAATTTCTACAGAAAACCTGATGCTGGTGGCCAGTGTGGCATGTGGAGCT 425
Db 760 TGCCCTTGTATGTGCGACATCCAGTAAAGCCCGGCGTTAATGTGGCCATATGGGCGCT 819
QY 426 GGTGATTTCTATGTGGTGATCCTGCTGCTCCCGTATGGAATCCATGAGGAATACAA 485
Db 820 GCTTTCGGTGGTGGTGTCTCTGTTGCCATCATGGGCTCAGCAAGTGGAGGATGAAGA 879
QY 486 TGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATCATCAA 545
Db 880 GATCGAGTGCCTGGTGGAGATCCCGCCCTCAGGACTATTTGGGGCCCTGTATTTGCCAT 939
QY 546 CTATATGATAGTCAATTTTGTCTAGCCGTTGCTGTGATTTCTGTGGTCTTCCAGGCTT 605
Db 940 CTGCACTCTCTTTTCTTCTTCAATCCCGGTTCTGATCATCTCTGTCTGTACAGCT 999
QY 606 CATCAT 612
Db 1000 CATGAT 1006

RESULT 13
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLER, C. Mark
; APPLICANT: OZENERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
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Patent No. 6103492  
GENERAL INFORMATION:  
APPLICANT: Yu, Lei  
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/889,108  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/305,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA005\WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 173..1273  
US-08-889-108-16

Query Match	6.5%; Score 59.8; DB 3; Length 1567;
Best Local Similarity	45.6%; Pred. No. 6.6e-08;
Matches	251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
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Db	
QY	330 GCCTCTACTTCGGCTGTGTGCATCGGGGGGCTCTCGGGGAAGCTCCCTCGCATGTATGTCA 389
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QY	122 TCCTCGTGGAAATGAACACCGGTCAGTGACCAACCATGGCGGTCATTAACCTTGGTGGTGG 181
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QY	390 TCTTCAGGCAACACAGATGAGACAGCTACCAACATTTACATATTATATCTGGCACTGG 449
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QY	182 TCCACAGCGGTTTTCTGTGTGACAGTGGCAATTCGCTTGACTACCTCATCAACAAGAAGCTT 241
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QY	510 GSCCATTTGGGAAATGCACTCTGCAAGACTGTGCATTGCTATCGACTACTACAACATGTTTA 569
Db	
QY	302 TCACGTTCTCTATTCTATGTGTGTGATCTGTGTCAACCAATCACTCATCTCTTTCAGTGGCA 361
Db	
QY	570 CCAGCACTTTTACTCTGACCGCCATGACCGGTAGACCGCTATGTGGCTATCTGCCACCCCTA 629
Db	
QY	362 AAGACAAAGTGGAAATCTACAGAAAATCTGATGCTGTGGCTGCCAGTGTGCATGTGGCA 421
Db	
QY	630 TCCGTGCGCCCTGATGTTTCGGHACATCCAGACAAAGCCCHAGGCTGTTAATGTGGCCATATGGG 689
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QY	422 CGCTCGGTGATTGTCAATTTGGTGTACCCCTGGTTGTCTCCCGGTATGGAAATCCCATAGGGAAT 481
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690 CCTCGGCTTCAGTGGTGGTCTCCTGTTGCCATCATGGGTTCCAGCACAAAGTGAAGATG 74
482 ACAATGAGGAGCAGCTGTTTTAAATTTCCAAAGAGCTTGCTTACACATATGTGAAAATCA 541
750 AAGAGATCGAGTGCCTGGTGGAGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATTGG 809
542 TCAACTATATCATAGTACATTTTGTGTCATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAGG 601
810 CCAATCTGCATCTTCTCTTTTCTTCTTCATCATCCCTGTGCTGATCATCTCTGTCCTGTACA 869
602 TCTTCATCAT 612
870 GCTCATGATT 890

RESULT 11
PCT-US94-10358-16
; Sequence 16, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 173..1273
; PCT-US94-10358-16

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	Query Match	6.5%	Score 59.8	DB 5	Length 1567
	Best Local Similarity	45.6%	Prod. No. 6.6e-08		
	Matches 251	Conservative 0	Mismatches 297	Indels 3	Gaps 17
QY	65	GCCTCTACTTCATAGTCTTATTGGCGGGCTGTGGG---	TGTCATTCCATCTTTTCC	121	
Db	330	GGCTCTACTTGGCTGTGTGATCGGGGGCTCTGGGGAAC	TCTCGTATGATGTC	389	
QY	122	TCTGGTGAAATGAACACCCGGTCTAGTGACCACCATCGCGGT	CTAATCAATGTGGTGG	181	
Db	390	TCCTCAGSCACCAAGATGAAGACAGCTACCAACATTTACAT	ATTAAATCTGGCACTGG	449	



382 CAGGCACCAAGATGAAGACTGCTACCAACATTTACATATTTAATCTGGCACTGGCTGA 441  
186 CAGCGTTTCTGCTCAGAGTGCCTTTTCGCTTGACCTACCTCATCAAGAGACTTGGAT 245  
442 TACCCCTGGCTTCTGCTGACACTGCCCTTCCAGGCGACAGACATCCTTCTGGGCTTCTGGCC 501  
246 GTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCTATGCTGCACATCCACATGTACTCTCAC 305  
502 ATTGGGAATGACATGTGCAAGACGCTCATTGCTATCGACTACTACAACATGTTTACCAG 561  
306 GTTCTTATCTATGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365  
562 CACTTTCATCTTGCAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 621  
366 CAAAGTGGAAATCTACAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425  
622 TGGCCTTGATGCTGCGACATCCAGTAAGCCGCGTATGTTGGCCATATGGCCCT 681  
426 GGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGT 485  
682 GGTCTCGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741  
486 TGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545  
742 GATCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801  
546 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605  
802 CTGATCTTCTCTTCT 861  
606 CATCAT 612  
862 CATGAT 868

## RESULT 9

US-08-292-694A-5  
Sequence 5, Application US/08292694A  
Patent No. 6319686  
GENERAL INFORMATION:  
APPLICANT: BELL, GRAEME  
APPLICANT: REISINE, TERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,694A  
FILING DATE: August 19, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20 May 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 July, 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/147,592  
FILING DATE: 5 No. 6319686member 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US94/05747  
FILING DATE: 20 May 1994

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 161..1261  
US-08-292-694A-5  
Query Match 6.5%; Score 59.8; DB 4; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 6e-08;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;  
Qy 9 CCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTCACACCCACCTTAATCAGCCT 68  
Db 262 CCTCAATGCTAGCCACAGTGCCTTCTGCCCCCTTGGACTCAGGTACCAATCGTGGGCT 321  
Qy 69 CTACTTTCATAGTGTATTTGGCGGGCTGTGGG---TGTCAATTTCCATTTTTCCTCT 125  
Db 322 CTACTTGGCTGTGTGATCGGGGGCTCTCTGGGAACCTGCTCGTATGATGTCATCCT 381  
Qy 126 GGTGAAATGAACACCCCGTCACTGACCAACCAATGGGGCTATTAACTTGTGGTGGTCCA 185  
Db 382 CAGGCACCAAGATGAAGACTGCTACCAACATTTACATATTTAATCTGGCACTGGCTGA 441  
Qy 186 CAGCGTCTTCTGCTGACAGTGCCTTTCCTCTGACCTACCTCATCAAGAGACTTTGGAT 245  
Db 442 TACCTGGTCTTGTGACACTGCCCTTCCAGGCGACAGACATCCTTCTGGGCTTCTGGCC 501  
Qy 246 GTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305  
Db 502 ATTTGGGAATGCACTGTGCAAGAGCGTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561  
Qy 306 GTTCTTATCTATGTGTGTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365  
Db 562 CACTTTCATTTGACTGCCATGAGTGTAGACCGTTATGTAGCTATCTGCCACCTATCCG 621  
Qy 366 CAAAGTGAATTTACAGAAATCTGCAATGTGTGGCTGCCAGTCTGCTGCTGCTGCTGCTGCTGCT 425  
Db 622 TGGCCTTGATGTTCCGACATCCAGTAAGCCGCGTAAATGGGCGCTTAAATGGGCGCTATGGGCGCT 681  
Qy 426 GGTGATGTCTATGTTGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485  
Db 682 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741  
Qy 486 TGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545  
Db 742 GATCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801  
Qy 546 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605  
Db 802 CTGATCTTCTCTTCT 861  
Qy 606 CATCAT 612  
Db 862 CATGAT 868

## RESULT 10

US-08-889-108-16  
; Sequence 16, Application US/08889108

NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1417:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1182 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 952059  
US-09-016-434-1417

Query Match 6.6%; Score 61; DB 4; Length 1182;  
Best Local Similarity 44.2%; Pred. No. 2.4e-08;  
Matches 351; Conservative 0; Mismatches 435; Indels 9; Gaps 2;

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QY 68 TCTACTTCATAGTCCTTATTGGCGGCTGGTGGGTGTC---ATTTCATTCCTTTCTCTCC 124
Db 207 TCTACTCCGAGTGTTCGTGGGCTGGTGGCAACTCGCTGGTCATGTCGTGATCA 266
QY 125 TGGTGAATAATGAACACCCGGTCACTGACCACTGGCGGTCAATTAACCTTGGTGGTCTC 184
Db 267 TCGATACACAAAGATGAAGACACCAACACATTTACATATTTAACTCGCTTTGGCAG 326
QY 185 ACAGCGTTTCTCTGACAGTGCATTCCTGCTTGACCTACCTCATCAAGAACATTTGGA 244
Db 327 ATGCTTTAGTTACTACAAACCATGCCCTTTCCAGAGTACGGTCTACTTGATGAATTCCTGGC 386
QY 245 TGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTACCTCA 304
Db 387 CTTTGGGATGCTGTGCAAGATATATTTCCATGTATTACTACAAATGTTACCA 446
QY 305 CGTTCCTATTCTATGTTGGTATCTGTGTCACAGATACCTCATCTTCTTCAAGTGCAAG 364
Db 447 GCATCTTTCACCTTGACCATGATGAGCTGGACCGCTACATTGGCGTGTGCCACCCCGTGA 506
QY 365 ACAAGTGGGAATTCACAGAAAATCTGCATCTGTGGCTGCCAGTGTGGCATGTGGACGC 424
Db 507 AGCGTTTGGACTTCGACACCCCTTGAAGGAAGATCATCAATATCTGATCTGCTGCTC 566
QY 425 TGGTG-----ATTGTCAITGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGG 478
Db 567 TGTGCTCATCTGTGGCATCTCTGCAATAGTCTCTGGAGGCACCAAGTCAGGGAAGACG 626
QY 479 AATACATGAGGACATGTTTAAATTTCAAGAGCTTGTGTACACATATGTGAATA 538
Db 627 TCGATGTCAATGATGTCTCTTGAGTTCACAGATGATGACTACTCTCTGGTGGACCTCT 686
QY 539 TCATCAACTATATGATAGTCATTTTGTCTATAGCCGTGTCTGTGATTTCTGTTGGTCTTCC 598
Db 687 TCAATGAAGATCTGGCTTCTCATCTTGGCTTGTGATCCCTGCTCATCATCATCTCT 746
QY 599 AGCTCTTCATATATGATGATGGTGCAGAGCTAGCCACTCTTTACTATCCACAGG 658
Db 747 GTACACCCGTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTTCTGGCTCCCGAGAGA 806
QY 659 AGTTCCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTC 718
Db 807 AAGATCGCAACCTGCGTAGGATCACCAGACTGCTGGTGGTGGTGGGTTTCTGTCG 866
QY 719 CCTACAGATCTTTAGGATCTATATCTTGAATGTTGTGAGCATTCCTAATGCTGTAAACA 778
Db 867 TCTGCTGGACTCCCAATTCATATTCCTGTTGGAGGCTCTGGGGAGCACCTCCACCA 926
QY 779 GCAAGGTGCAATTTTATAAGAAATCTTCTTGTAGTGTAAAGCAATTAGCTGTATGATT 838
Db 927 GCACAGTCTCTCTCCAGCTATTACTTTCTGCAATCGCTTTAGGCTATACCAAGTAGCC 986
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QY 839 TGCTTCTCTTTGTCT 853
Db 987 TGAATCCCATTTCTCT 1001

RESULT 8
US-08-147-592A-5
; Sequence 5, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 72210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 161..1261
; US-08-147-592A-5
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Query Match 6.5%; Score 59.8; DB 3; Length 1330;  
Best Local Similarity 44.8%; Pred. No. 6e-08;  
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

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QY 9 CCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTAATCAGCCT 68
Db 262 COTCAATGCTAGCCACACAGTGCCTTCTCCCTTTGGACTCAAGGTCAACATCGTGGGCT 321
QY 69 CTACTTTCATAGTCTTATTGGCGGCTGGTGGG---TGTCAATTTCCATTCCTTTCTCTCT 125
Db 322 CTACTTGGCTGTGTCATCGGGGGCTCTCTGGGAACCTGCTCGTCAATGATCATCCT 381
QY 126 GGTGAATGAACACCCCGGTGAGTGACCAATGGCGGTCAATTAACCTTGGTGGTGCCA 185
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;; PRIOR APPLICATION NUMBER: 60/093,002  
;; PRIOR FILING DATE: 1996-07-16  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 14  
;; LENGTH: 1134  
;; TYPE: DNA  
;; ORGANISM: homo sapiens  
US-09-743-871B-14

Query Match 8.0%; Score 73.2; DB 4; Length 1134;  
Best Local Similarity 46.8%; Pred. No. 5e-12;  
Matches 231; Conservative 0; Mismatches 263; Indels 0; Gaps 0;  
QY 118 TTCCTCTGCTGAAATGAACACCCGGTCAGTGACACACATGGCGGTCAATTAACCTGGT 177  
Db 223 TGCCTTGTGATGCACACCAAAATGAAGACAGCCACCAATATTTACATCTTTAACTGGCC 282  
QY 178 GTGGTCCACAGGTTTTCTGTGTGACAGTGCCATTCGCTTGACCTACCTCATCAAGAAG 237  
Db 293 CTGGCGGACACTCTGTGCTGTGAGCTGCGCTTCCAGGCGACGGACATCTCTGGGC 342  
QY 238 ACTTGGATGTTTGGGCTGCGCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATG 297  
Db 343 TTCTGCGGCTTTGGGAATGCGGTGTGCAAGACAGTCATTGCCATTGACTACTACAACATG 402  
QY 298 TACCTCACGTTCTTATTTATGTGTGATCTCTGTGTCACGATACCTCATCTCTTCAAG 357  
Db 403 TTCACGACACTTCCACCTTAATCTGCTGATGAGTGAGTGAGTATGCTATGAGCCATCTGCCAC 462  
QY 358 TGCAAGACAAAGTGGAAATTTACAGAAATTCATGCTGTGGTGGCGATGCTGGCATG 417  
Db 463 CCCATCCGTGCGCTCGAGTCCGCGCTCCAGCAAGCCAGGCTGTCAATGTGGCCATC 522  
QY 418 TGGAGCTGCTGATGTCATGTTGGTACCCCTGGTGTGCTCCCGTATGGAATCCATGAG 477  
Db 523 TGGGCGCTGCGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582  
QY 478 GAATACAAATGAGGACACTGTTTTAAATTTCAAGAGCTTGTCTACACATATGTGAAA 537  
Db 583 GATGAAGAGATCGAGTCTGCTGTGGAGATCCCTACCCCTCAGGATTAATGCGGCGCGGTG 642  
QY 538 ATCATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597  
Db 643 TTGGCATCTGATCTTCT 702  
QY 598 CAGGCTTTCATCAT 611  
Db 703 TACAGCCTCATGAT 716

RESULT 6  
US-09-743-871B-13  
; Sequence 13, Application US/09743871B  
; Patent No. 6627734  
; GENERAL INFORMATION:  
; APPLICANT: Memorial Sloan-Kettering Cancer Center  
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUS  
; FILE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE  
; FILE REFERENCE: 830002-2001.1  
; CURRENT APPLICATION NUMBER: US/09/743,871B  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US99/15977  
; PRIOR FILING DATE: 1997-07-15  
; PRIOR APPLICATION NUMBER: 60/093,002  
; PRIOR FILING DATE: 1996-07-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 1177  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-743-871B-13

Query Match 7.6%; Score 70.2; DB 4; Length 1177;  
Best Local Similarity 46.6%; Pred. No. 4.1e-11;  
Matches 225; Conservative 0; Mismatches 258; Indels 0; Gaps 0;  
QY 129 GAAATGAACACCCGGTCAGTGACACCATGGCGGTCAATTAACCTGGTGGTGGTGGTGGTGGT 188  
Db 277 GCACACCAAAATGAAGACAGCCACCAATATTTACATCTTTAACTGGCGCTGGCGGACAC 336  
QY 189 CGTTTTTCTGTGACAGTGGCCATTTGCTTGACCTACCTACCTACCTACCTACCTACCTACCTAC 248  
Db 337 TCTGGTCTGCTGACGCTGCGCTTCCAGGCGCAGGACATCTCTCTGGGCTTCTGGCGGTT 396  
QY 249 TGGGCTGCGCTTCTGCAAAATTTGTGAGTGCATGCTGTGCATCCACATCCACATCTACCTCACGTT 308  
Db 397 TGGGAATGCGCTGTGACAGCAGTCTATGCCATTGACTACTACCAACATGTTCAACGACAC 456  
QY 309 CCTATTCTATGTGGTGAATCCTGGTACCAGATACCTCATCTCTTCTCAAGTGCAAGACAA 368  
Db 457 CTTACCCCTAACTGCGCATGAGTGTGGATCGCTATGTAGCCATCTGCCACCCCATCCGTGC 516  
QY 369 AGTGGATTTCTACAGAAACTGCATGCTGTGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGTGT 428  
Db 517 CTTGAGCTGCGCAGCTCCAGCAAGCCAGGCTGTCAATGTGGCCATCTGGGCGCTGCG 576  
QY 429 GATTGTCAATGTGGTACCCCTGCTGTCTCCCGGTATGGAATCCATGAGGAATACAATGA 488  
Db 577 CTCTGTGTCGGGTGTTCCCGTTGCCATCATGGCTCGGCACAGGTCGAGGATGAAGAGAT 636  
QY 489 GGAGCACTGTTTAAATTTCAAGAGAGCTTGTCTTACACATATGTGAAATCATCAACTA 548  
Db 637 CGAGTCCCTGGTGGAGATCCCTACCCCTCAGGATTAATGCGGCGCGGCTGTTGCGCCATCTG 696  
QY 549 TATGATAGTCAATTTTGTCTATAGCCGTTGCTGTGATCTTGTGTTGCTTCCAGGCTCTTCAT 608  
Db 597 CATCTTCT 756  
QY 609 CAT 611  
Db 757 GAT 759

RESULT 7  
US-09-016-434-1417  
; Sequence 1417, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1417:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1973 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9471316  
US-09-023-655-1417

Query Match 8.3%; Score 76.4; DB 4; Length 1973;  
Best Local Similarity 46.7%; Pred. No. 7.4e-13;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;  
QY 94 CTGGTGGGTGTCATTTCCATTTCTTCTCTCTGTTGAAATGAACACCCGGTCTAGTGACC 153  
DB 376 CTGGGGAATGCTCTTGTGTCATGTACGTATCTCTCAGGCACACCAAAATGAAGACGCCACC 435  
QY 154 ACCATGGCGGTGTCATTAACCTTGTTGGTGTCCACAGCGTTTCTCTGCTCAGACGTGCCATTT 213  
DB 436 AATATTACATCTTTAACTGTGCTGCGCCCTGCGGACACTCTGTGCTGCTGCTGCTGCTGCT 495  
QY 214 CGCTTGACCTACCTCATCAAGAGACTTGGATGTTGGTGGTCCCTCTCTGCAAAATTTGTG 273  
DB 496 CAGGCAACGGACATCTCTCTGGGCTTCTGGCGTTTGGGAATGCGCTGTGCAAGACAGTC 555  
QY 274 AGTGCATGCTGCATCCACATGACCTCAGTTCTCCTATCTATGCTGCTGCTGCTGCTGCTGCT 333  
DB 556 ATTGCGATGTACTATCAACATGTTCCACGACCTTCCACCTTAACCTGCTGCTGCTGCTGCTGCT 615  
QY 334 ACCAGATACCTCATCTTCTTCAAGTGCAAGAACAAAGTGAATTTCTACAGAAATCTGCAT 393  
DB 616 GATCGCTATGTAGCCATCTGCCACCCCATCGTGGCCCTCGACGTCGACGTCACGTCACGAAA 675  
QY 394 GCTGTGGCTGCAGTGTGGCATGTGGAGCGTGTGGTGTATGTATGCTGCTGCTGCTGCTGCTGCT 453  
DB 676 GCCCAGGCTGTCAATGTGGCCATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735  
QY 454 GTCTCCCGTATGGAATCCATGAGGAATACATGAGGAGCACTGTTTAAATTTTCAAAA 513  
DB 736 ATCATGGGCTCGGACAGGTGAGGATGAGAGATCGAGTGGCTGGTGGAGATCCCTACC 795  
QY 514 GAGCTTGCTTACACATATGTGAAATCATCACTATATGATAGTCAATTTTGTGCTAGACC 573  
DB 796 CCTCAGGATTAAGTGGGCGCGGTGTTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855  
QY 574 GTTGTGCTGATCTGTTGCTCTCCAGGCTTTCATCAT 611  
DB 856 CCCGTGCTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893

RESULT 4  
US-09-976-594-171  
Sequence 171, Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:

APPLICANT: Furness, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 171  
LENGTH: 3205  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 222181.1  
US-09-976-594-171

Query Match 8.3%; Score 76.4; DB 4; Length 3205;  
Best Local Similarity 46.7%; Pred. No. 9.8e-13;  
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;  
QY 94 CTGGTGGGTGTCATTTCCATTTCTTCTCTCTGTTGAAATGAACACCCGGTCTAGTGACC 153  
DB 450 CTGGGGAATGCTCTTGTGTCATGTACGTATCTCTCAGGCACACCAAAATGAAGACGCCACC 509  
QY 154 ACCATGGCGGTGTCATTAACCTTGTTGGTGTCCACAGCGTTTCTCTGCTGACAGTGCATTT 213  
DB 510 AATATTACATCTTTAACTGTGCTGCGCCCTGCGGACACTCTGTGCTGCTGCTGCTGCTGCTGCT 569  
QY 214 CGCTTGACCTACCTCATCAAGAGACTTGGATGTTGGTGGTCCCTCTCTGCAAAATTTGTG 273  
DB 570 CAGGCAACGGACATCTCTCTGGGCTTCTGGCGCTTGGGGAATGCGCTGTGCAAGACAGTC 629  
QY 274 AGTGCATGCTGCATCCACATGACCTCAGTTCTCCTATCTATGCTGCTGCTGCTGCTGCTGCTGCT 333  
DB 630 ATTGCGATGTACTATCAACATGTTCCACGACCTTCCACCTTAACCTGCTGCTGCTGCTGCTGCT 699  
QY 334 ACCAGATACCTCATCTTCTTCAAGTGCAAGAACAAAGTGAATTTCTACAGAAATCTGCAT 393  
DB 690 GATCGCTATGTAGCCATCTGCCACCCCATCGTGGCCCTCGACGTCGACGTCGACGAAA 749  
QY 394 GCTGTGGCTGCAGTGTGGCATGTGGAGCGTGTGGTGTATGTATGCTGCTGCTGCTGCTGCTGCTGCT 453  
DB 750 GCCCAGGCTGTCAATGTGGCCATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
QY 454 GTCTCCCGTATGGAATCCATGAGGAATACATGAGGAGCACTGTTTAAATTTTCAAAA 513  
DB 810 ATCATGGGCTCGGACAGGTGAGGATGAGAGATCGAGTGGCTGGTGGAGATCCCTACC 869  
QY 514 GAGCTTGCTTACACATATGTGAAATCATCACTATATGATAGTCAATTTTGTGCTAGACC 573  
DB 870 CCTCAGGATTAAGTGGGCGCGGTGTTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929  
QY 574 GTTGTGCTGATCTGTTGCTCTCCAGGCTTTCATCAT 611  
DB 930 CCCGTGCTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967

RESULT 5  
US-09-743-871B-14  
Sequence 14, Application US/09743871B  
Patent No. 6627734  
GENERAL INFORMATION:  
APPLICANT: Memorial Sloan-Kettering Cancer Center  
TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUSE  
FILE REFERENCE: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE  
CURRENT APPLICATION NUMBER: US/09/743,871B  
CURRENT FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: PCT/US99/15977  
PRIOR FILING DATE: 1997-07-15





NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/823,114  
FILING DATE: 29-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/148,351  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20526,22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1805 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..1119  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-823-114-18

Query Match	8.3%;	Score 76.4;	DB 9;	Length 1805;
Best Local Similarity	46.7%;	Fred. No. 4.6e-12;		
Matches 242;	Conservative 0;	Mismatches 276;	Indels 0;	Gaps 0;
QY	94	CTGGTGGGTGCATTTCATTTCCATTCCTTCTCCTGGTGAATGAACACCGGTCAGTGACC	153	
Db	208	CTGGGGAAGTGCCTTGTCTATGTACGTATCTCTCAGGCACACCAAAATGAAGACAGCCACC	267	
QY	154	ACCATGGCGGTCAATTAATCTGGTGGTGCACAGCGTTTTCTGTGACAGTGCATTT	213	
Db	268	AATAATTTACATCTTTAACTCGGCTCGGCCACACTCTGGTCTGTGACGCTGCCTTC	327	
QY	214	CGCTTGACCTACCTCATCAAGAAGACATTGGATGTTTGGGCTGCCCTTCCTGCAAAATTTGTG	273	
Db	328	CAGGCGACGGACATCCTCTCTGGGCTTCGGCCGTTTGGGAATCGCTGTGCAAGACAGTC	387	
QY	274	AGTGCCATGCTGCACATCCACATGACCTACAGTTCCTATTCATGTGGTGAATCCTGGTC	333	
Db	388	ATTGGCAATGACTACTACAAGATGTTCAACAGCACCTTCACCCCTAACTGCCATGAGTGTG	447	
QY	334	ACCATATACCTCATCTCTTCAAGTGCAGAGACAAAGTGGAAATCTTACAGAAAATCGGAT	393	
Db	448	GATCGCTATGTAGCCATCTGCCACCCCATCCGTGCCCTCGACCTCGCAGCTCCAGCAAA	507	
QY	394	GCTGTGGCTGCCAGTGTGGCATGTGACGCTGGTGAATGTCTCATGTGTGTAACCCCTGGTT	453	
Db	508	GCCAGGCTGTCAATGTGGCCATCTGGGCCCTCGCCCTCTGTTGTCGGTGTTCCTCGTGGC	567	
QY	454	GTCTCCCGTATGGAAATCCATGAGGAATACAAATGAGGAGCACTGTTTTAAATTTACAAA	513	
Db	568	ATCATGGGCTCGCACAGGTCCAGAGATGAAGAGATCGAGTGCCTGGTGAGATCCCTACC	627	
QY	514	GAGCTTGTGTTACACATATGTGAAAATCATCAACTATATGATAGTCAATTTTTGTCTATAGCC	573	





121 CTCCTGGTGAATAACACACCGGTCAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGT 180  
Db  
145 CTCCTGGTGAATAACACACCGGTCAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGT 204  
Qy  
161 GTCCACAGCGTTTCTGCTGACAGTGCATTCGCTTGACCTACCTCATCAAGAGACT 240  
Db  
205 GTCCACAGCGTTTCTGCTGACAGTGCATTCGCTTGACCTACCTCATCAAGAGACT 264  
Qy  
241 TGGATGTTTGGGCTGCCCTCTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300  
Db  
265 TGGATGTTTGGGCTGCCCTCTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 324  
Qy  
301 CTCAGTTCCTATTCTATGTTGGTGTATCTCTGTCAGCAGATACCTCATCTTCAAGTGC 360  
Db  
325 CTCAGTTCCTATTCTATGTTGGTGTATCTCTGTCAGCAGATACCTCATCTTCAAGTGC 384  
Qy  
361 AAAGCAAAAGTGAATCTTACAGAAAATGTCATGCTGGCTGCCAGTGGCTGGCATGTGG 420  
Db  
385 AAAGCAAAAGTGAATCTTACAGAAAATGTCATGCTGGCTGCCAGTGGCTGGCATGTGG 444  
Qy  
421 AGCTGTGATGTTGTCATGTTGTACCCCTGTTGTCACCAAGAGCTTGTACACATATGTGAATC 480  
Db  
445 AGCTGTGATGTTGTCATGTTGTACCCCTGTTGTCACCAAGAGCTTGTACACATATGTGAATC 504  
Qy  
481 TACATAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTACACATATGTGAATC 540  
Db  
505 TACATAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTACACATATGTGAATC 564  
Qy  
541 ATCAACTATATGATAGTCAATTTTGTATAGCGTGTGCTGATCTGTTGGTCTTCCAG 600  
Db  
565 ATCAACTATATGATAGTCAATTTTGTATAGCGTGTGCTGATCTGTTGGTCTTCCAG 624  
Qy  
601 GTCTTCATCATATGTCATGTCAGAGCTACGCCACTTCTTACTATCCACAGGAG 660  
Db  
625 GTCTTCATCATATGTCATGTCAGAGCTACGCCACTTCTTACTATCCACAGGAG 684  
Qy  
661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720  
Db  
685 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 744  
Qy  
721 TACAGTTCCTTAGATCTATTAATGATGTTGTAGCGCATTCATCCATGCTGTAAACG 780  
Db  
745 TACAGTTCCTTAGATCTATTAATGATGTTGTAGCGCATTCATCCATGCTGTAAATG 804  
Qy  
781 AAGGTTGCAATTTTAAACGAAATCTTCTTGTAGTGTAAACGAAATAGCTGTATGATTG 840  
Db  
805 AAGGTTGCAATTTTAAACGAAATCTTCTTGTAGTGTAAACGAAATAGCTGTATGATTG 864  
Qy  
841 CTCTCTTTGCTTTGGGGAGCCATGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900  
Db  
865 CTCTCTTTGCTTTGGGGAGCCATGTTTAAAGCAAAAGATAATGGCTTATGGAAT 924  
Qy  
901 TGTGTTTGTGCGGT 915  
Db  
925 TGTGTTTGTGCGGT 939

PRIOR FILING DATE: 2002-08-22  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 810  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-366-504-1

Query Match 61.1%; Score 560.8; DB 15; Length 810;  
Best Local Similarity 81.1%; Pred. No. 8.3e-161;  
Matches 652; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTTGGAGATCCTATAGTGACACCCCACTTA 60  
Db 1 ATGCTGGATATAATACCTCTGAGAAATTCCTTGTGACCCCTATAGTGACACCCCACTTA 60  
Qy 61 ATCAGCCTCTACCTTACATAGTGTCTTATTTGGCGGCTGCTGGGTGTCATTTCCATCTTTTC 120  
Db 61 ACATCGATTTACCTTACATAGTGTCTTATTTGGAGACTGGTAGTCTCATCTCCATCTTTC 120  
Qy 121 CTCTGGTGAATAAGAACCCCGGTGAGTGAACCAACATGGCGGTCAATTAATCTGGTGGT 180  
Db 121 TTGCTGGTGAATAAGAACCTCACGTTGAGTGAACCAACATGGCTGTATCAACCTCGTGGT 180  
Qy 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCGTTCGCTTACCTACCTCATCAAGAGACT 240  
Db 181 GTTCATGGGCTCTTCTTACTGACGGTGCCTTTCCGCTTGGCATACCTCATCAAGAGACT 240  
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300  
Db 241 TGGACGTTTGGATTAACCTTCTGCAAAATTTGTAGTGCCATGTTACATATCCACATGTAC 300  
Qy 301 CTACGTTTCTTATCTATGTTGGTGTATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360  
Db 301 CTACGTTTCTTCTTCTACGTTGGTGTATGATAGTATCAGATACCTCATCTTCTTCAAGCGT 360  
Qy 361 AAAGCAAAAGTGAATTTCTACAGAAAATGTCATGCTGGCTGCCAGTGGCTGATGTGG 420  
Db 361 AGAGCAAAAGTGAATTTCTATAGAAAATTTGCAATGCAATGCTGCAAGTTCGCTGCAATG 420  
Qy 421 ACGTGTGATGTTGTCATGTTGGTGTATCCCTGTTGCTCCGCTATGGAATCCATGAGGAA 480  
Db 421 CTCTGCTGATTTGTTATTTGTTGTCGCTTGGTGGTTCCTCAGTATGGAATAGCGAAGAA 480  
Qy 481 TACAATGAGAGACACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540  
Db 481 TACAATGAGCAACAGTGTCTTATAGTTCCATAAAGAACTTGGCCATGATCTGTGCGAGTT 540  
Qy 541 ATCAACTATATGATAGTCAATTTTGTGTCATAGCCGTTGCTGTGATTCGTGTTGCTTCCAG 600  
Db 541 ATCAACTATATGATAGTCAATTTGTTGTATAGCTGTTGCGTGTGATTCCTTGGGTTTCCAG 600  
Qy 601 GTCTTCATCATATGTTGATGTTGAGAGCTACGCCACTCTTTTACTATCCACAGGAG 660  
Db 601 GTCTTCATCATATGTTGATGTTGAGAGCTTTCGCCACTCTTACTATCCACAGGAG 660  
Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTGTCATCTTGTGTTTCTTCTTCC 720  
Db 661 TTCTGGGCACTGAAAATCTTTTCTTATAGGTATCATTTATTTGTTTCTTCTTCC 720  
Qy 721 TACAGTTCCTTAGGATCTATTAATGATGTTGTGACCGATTCCTCAATGCTGTAAACG 780  
Db 721 TACCAGTTCCTTAGGATTTATTAATGATGTTGTGAGCAATTCCTCAAGAGCTGTAAAAAC 780  
Qy 781 AAGGTTGCAATTTTAAACGAAATC 804  
Db 781 AAGGTTGCAATTTTAAACGAAATC 804

RESULT 13  
US-09-782-974C-21/c  
; Sequence 21, Application US/09782974C

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Db 12260 TACGAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCCGTGTAAACAGC 12319
Qy 781 AAGTTGCAATTTTATACGAATCTCTTGAGTGTAAACGAATTAAGTGTGCTATGATTTG 840
Db 12320 AAGTTGCAATTTTATACGAATCTCTTGAGTGTAAACGAATTAAGTGTGCTATGATTTG 12379
Qy 841 CTTCTCTTTGCTCTTTGGGGGAACCAATCTGTTTAAAGCAAAAGATTAATTCGGCTTATGGAAT 900
Db 12380 CTTCTCTTTGCTCTTTGGGGGAACCAATCTGTTTAAAGCAAAAGATTAATTCGGCTTATGGAAT 12439
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 12440 TGTGTTTTGTGCCGTTAG 12457

RESULT 10
US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCES: MP12001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Query Match 99.8%; Score 916.4; DB 15; Length 1684;
Best Local Similarity 99.9%; Pred. No. 1.3e-269;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 171 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 230
Qy 61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGTCATTTCCCATTTCTTTTC 120
Db 231 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGTCATTTCCCATTTCTTTTC 290
Qy 121 CTCCTGGTGAATAAGAACCCCGGTGAGTGCACACCAATGCGGTGATTAACCTTGTGGTG 180
Db 291 CTCCTGGTGAATAAGAACCCCGGTGAGTGCACACCAATGCGGTGATTAACCTTGTGGTG 350
Qy 181 GTCCACAGCGTTTTCTGCTGACAGTGCATTTTCGCTTACCTTACCTCATCAAGAAGACT 240
Db 351 GTCCACAGCGTTTTCTGCTGACAGTGCATTTTCGCTTACCTTACCTCATCAAGAAGACT 410
Qy 241 TGGATTTTGGGTGCGCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 411 TGGATTTTGGGTGCGCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 470
Qy 301 CTCACGTTCTTATCTATGTTGGTATCCTGGTCCACAGATACCTCATCTTCTCAAGTGC 360
Db 471 CTCACGTTCTTATCTATGTTGGTATCCTGGTCCACAGATACCTCATCTTCTCAAGTGC 530
Qy 361 AAAGCAAAAGTGGAAATTTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 420
Db 531 AAAGCAAAAGTGGAAATTTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 590
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Qy 421 ACGTGGTGTGATTCATTCGTTACCCCTGGTTGTTCTCCCGGTATGGAATCCCATGAGAA 480
Db 591 ACGTGGTGTGATTCATTCGTTACCCCTGGTTGTTCTCCCGGTATGGAATCCCATGAGAA 650
Qy 481 TACAATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGTCTACACATATGTGAAATC 540
Db 651 TACAATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGTCTACACATATGTGAAATC 710
Qy 541 ATCAACTATATGATGATTCATTTTGTCTACAGCGTGTCTGTGATCTCTGTTGGTCTTCAG 600
Db 711 ATCAACTATATGATGATTCATTTTGTCTACAGCGTGTCTGTGATCTCTGTTGGTCTTCAG 770
Qy 601 GTCCTTCATCATTCATTCGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660
Db 771 GTCCTTCATCATTCATTCGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 830
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTGATCTCTGTTGTTCTTCCTCC 720
Db 831 TTCTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTGATCTCTGTTGTTCTTCCTCC 890
Qy 721 TACCAGTCTCTTAGGATCTATTACTTCAATGTTGTGACGCAATTCGAATGCTGTAAACAGC 780
Db 891 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAGCAGC 950
Qy 781 AAGTTGCAATTTTATAACGAATCTCTTCTGAGTGTAAACGAATAGCTGCTATGATTG 840
Db 951 AAGTTGCAATTTTATAACGAATCTCTTCTGAGTGTAAACGAATAGCTGCTATGATTG 1010
Qy 841 CTTCTCTTTGCTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATTCGCTTATGGAAT 900
Db 1011 CTTCTCTTTGCTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATTCGCTTATGGAAT 1070
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 1071 TGTGTTTTGTGCCGTTAG 1088

RESULT 11
US-10-085-233B-3
; Sequence 3, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCES: MP12001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(939)
US-10-085-233B-3

Query Match 99.5%; Score 913.4; DB 15; Length 939;
Best Local Similarity 99.9%; Pred. No. 7.2e-269;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 25 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 84
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGCTGGTGGGTGTCAATTTCCATTTCTTTTC 120
Db 85 ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGCTGGTGGGTGTCAATTTCCATTTCTTTTC 144
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Db 267 TGGATGTTGGCTGCCCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 326  
Qy 301 CTCAGTTCTTATCTATGTTGGTGTGATCTGCTGCTACCATACCTCATCTTCTTCAAGTGC 360  
Db 327 CTCAGTTCTTATCTATGTTGGTGTGATCTGCTGCTACCATACCTCATCTTCTTCAAGTGC 386  
Qy 361 AAAGACAAAGTGGAAATCTACAGAAAATCTGATGCTGTGGCTGCCAGTGTGGCATGTGG 420  
Db 387 AAAGACAAAGTGGAAATCTACAGAAAATCTGATGCTGTGGCTGCCAGTGTGGCATGTGG 446  
Qy 421 ACGTGTGATGTGATCTGTTGGTGTGATGCTGTGGCTGCCAGTGTGGCATGTGGCATGTGG 480  
Db 447 ACGTGTGATGTGATCTGTTGGTGTGATGCTGTGGCTGCCAGTGTGGCATGTGGCATGTGG 506  
Qy 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540  
Db 507 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 566  
Qy 541 ATCAACTATATGATGATCTATTTTGTGATAGCCGTTGCTGTGATCTGTTGGTCTTCCAG 600  
Db 567 ATCAACTATATGATGATCTATTTTGTGATAGCCGTTGCTGTGATCTGTTGGTCTTCCAG 626  
Qy 601 GTCCTTCATCATATGATGATCTGTTGGTGTGATGCTGTGGCTGCCAGTGTGGCATGTGG 660  
Db 627 GTCCTTCATCATATGATGATCTGTTGGTGTGATGCTGTGGCTGCCAGTGTGGCATGTGG 686  
Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTTGTGTTTGTCTTCTTCCC 720  
Db 687 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTTGTGTTTGTCTTCTTCCC 746  
Qy 721 TACCAAGTTCTTATAGATCTATTTTGTGATGATGCTGTGGCTGCCAGTGTGGCATGTGG 780  
Db 747 TACCAAGTTCTTATAGATCTATTTTGTGATGATGCTGTGGCTGCCAGTGTGGCATGTGG 806  
Qy 781 AAGGTTGATTTTATAGCAAAATCTTCTGATGATGATGATGATGATGATGATGATGATG 840  
Db 807 AAGGTTGATTTTATAGCAAAATCTTCTGATGATGATGATGATGATGATGATGATGATG 866  
Qy 841 CTTCTCTTGTCTTGTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGAAAT 900  
Db 867 CTTCTCTTGTCTTGTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGAAAT 926  
Qy 901 TGTGTTTGTGCGGTTAG 918  
Db 927 TGTGTTTGTGCGGTTAG 944

## RESULT 9

US-10-292-798-1007  
; Sequence 1007, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1007  
; LENGTH: 113306  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; LOCATION: source

FEATURE: (1)..(113306)  
LOCATION: (1)..(113306)  
NAME/KEY: CDS  
LOCATION: (201)..(207)  
FEATURE: (201)..(207)  
NAME/KEY: CDS  
LOCATION: (11526)..(12452)  
FEATURE: (11526)..(12452)  
NAME/KEY: CDS  
LOCATION: (37954)..(38097)  
FEATURE: (37954)..(38097)  
NAME/KEY: CDS  
LOCATION: (98732)..(98784)  
FEATURE: (98732)..(98784)  
NAME/KEY: CDS  
LOCATION: (112891)..(113106)  
FEATURE: (112891)..(113106)  
US-10-292-798-1007  
Query Match 100.0%; Score 918; DB 16; Length 113306;  
Best Local Similarity 100.0%; Pred. No. 7,1e-269; Indels 0; Gaps 0;  
Matches 918; Conservative 0; Mismatches 0;  
Qy 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCCTATAGTGCACACCCCACTTA 60  
Db 11540 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCCTATAGTGCACACCCCACTTA 11599  
Qy 61 ATCAGCCTCTACTTCAATGATGCTTATTTGGGGCTGGTGGGTGTCATTTCCATCTTTTC 120  
Db 11600 ATCAGCCTCTACTTCAATGATGCTTATTTGGGGCTGGTGGGTGTCATTTCCATCTTTTC 11659  
Qy 121 CTCCTGTGAAATGAACACCCGGTCAGTGACCAATGGCGTCATTAACTTTGGTGGTG 180  
Db 11660 CTCCTGTGAAATGAACACCCGGTCAGTGACCAATGGCGTCATTAACTTTGGTGGTG 11719  
Qy 181 GTCACAGCGTTTCTGTGACAGTGCCTATTTGGTGGTGGTGCCTATCTCATCAAGAAAGCT 240  
Db 11720 GTCACAGCGTTTCTGTGACAGTGCCTATTTGGTGGTGGTGCCTATCTCATCAAGAAAGCT 11779  
Qy 241 TGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCTATGTCACATCCACATGTAC 300  
Db 11780 TGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCTATGTCACATCCACATGTAC 11839  
Qy 301 CTCACGTTCCATTTATGATGATGATCCTGGTGCACAGATACCTCATCTTCTTCAAGTGC 360  
Db 11840 CTCACGTTCCATTTATGATGATGATCCTGGTGCACAGATACCTCATCTTCTTCAAGTGC 11899  
Qy 361 AAAGACAAAGTGGAAATCTACAGAAAATCTGCTGCTGCTGCCAGTGCCTGCATGTGC 420  
Db 11900 AAAGACAAAGTGGAAATCTACAGAAAATCTGCTGCTGCTGCCAGTGCCTGCATGTGC 11959  
Qy 421 ACGTGTGATGCTCATTTGTGATGATGATCCTGGTGTGCTCCCGGTATGGAATCCATGAGGAA 480  
Db 11960 ACGTGTGATGCTCATTTGTGATGATGATCCTGGTGTGCTCCCGGTATGGAATCCATGAGGAA 12019  
Qy 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540  
Db 12020 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 12079  
Qy 541 ATCAACTATATGATGATCTATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 12080 ATCAACTATATGATGATCTATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12139  
Qy 601 GTCTTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
Db 12140 GTCTTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12199  
Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTGATCCTCTGTTTGTGTTTCTTCCC 720  
Db 12200 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTGATCCTCTGTTTGTGTTTCTTCCC 12259  
Qy 721 TACCAGTTCTTTAGGATCTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 780

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; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: source
; LOCATION: (1)..(1318)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1118)
; US-10-017-161-1193

Query Match      100.0%; Score 918; DB 15; Length 1318;
Best Local Similarity 100.0%; Pred. No. 3.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCAAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 60
DB 201 ATGCTGGCCAAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 260

QY 61 ATCAGGCTCTACTTCATAGTCTTATTGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 120
DB 261 ATCAGGCTCTACTTCATAGTCTTATTGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 320

QY 121 CTCCTGGTGAANAATGAACCCCGGTGACGACCAATGCGGTCAATTAATCTGGTGGTG 180
DB 321 CTCCTGGTGAANAATGAACCCCGGTGACGACCAATGCGGTCAATTAATCTGGTGGTG 380

QY 181 GTCCACAGCGTTTTCGTGTCAGAGTCCATTTTCGTTGACCTTACCTCATCAAGAGACT 240
DB 381 GTCCACAGCGTTTTCGTGTCAGAGTCCATTTTCGTTGACCTTACCTCATCAAGAGACT 440

QY 241 TGGATGTTGGGTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
DB 441 TGGATGTTGGGTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 500

QY 301 CTCACGTTCTATTCTATGTTGGTGATCCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
DB 501 CTCACGTTCTATTCTATGTTGGTGATCCTGTCACAGATACCTCATCTTCTTCAAGTGC 560

QY 361 AAAGACAAATGGAATCTTACAGAAATCTGCTGTGGCTGCCAGTGTGCTGCATGTGG 420
DB 561 AAAGACAAATGGAATCTTACAGAAATCTGCTGTGGCTGCCAGTGTGCTGCATGTGG 620

QY 421 ACCTGTGTGATTCATTTGTTGGTGTACCCCTGTTGTCTCCGGTATGGAATCCATGAGGAA 480
DB 621 ACCTGTGTGATTCATTTGTTGGTGTACCCCTGTTGTCTCCGGTATGGAATCCATGAGGAA 580

QY 481 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGCTTTACACATATGTGAAATC 540
DB 681 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGCTTTACACATATGTGAAATC 740

QY 541 ATCAACTATATGATGATCATTTTGTATAGCCGTTGCTGTGATTTCTGTTGTTCTTCCAG 600
DB 741 ATCAACTATATGATGATCATTTTGTATAGCCGTTGCTGTGATTTCTGTTGTTCTTCCAG 800

QY 601 GTCTTCATCATATTATGTTGATGTTGCGAAGCTACGCCACTCTTTACTATCCACACGAGG 660
DB 801 GTCTTCATCATATTATGTTGATGTTGCGAAGCTACGCCACTCTTTACTATCCACACGAGG 860

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTGTTGTTTCTTCCCTCC 720
DB 861 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTGTTGTTTCTTCCCTCC 920

QY 721 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGATTTCCAAATGCTGTAAACAGC 780
DB 921 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGATTTCCAAATGCTGTAAACAGC 980

QY 781 AAGTTGCATTTTATACGAAATCTTCTGAGTGTAAACAGAAATAGCTCTATGATTTG 840
DB 981 AAGTTGCATTTTATACGAAATCTTCTGAGTGTAAACAGAAATAGCTCTATGATTTG 1040
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QY 841 CTTCTCTTTGTCTTTGGGGAAGCCATTGTTTAAAGCAAAAGATAATTGCTTTATGGAAT 900
DB 1041 CTTCTCTTTGTCTTTGGGGAAGCCATTGTTTAAAGCAAAAGATAATTGCTTTATGGAAT 1100

QY 901 TGTGTTTTGTGCGGTTAG 918
DB 1101 TGTGTTTTGTGCGGTTAG 1118
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## RESULT 8

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US-09-782-974C-81
; Sequence 81, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Patodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-782-974C-81
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Query Match      100.0%; Score 918; DB 10; Length 2525;
Best Local Similarity 100.0%; Pred. No. 5.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCAAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 60
DB 27 ATGCTGGCCAAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 86

QY 61 ATCAGGCTCTACTTCATAGTCTTATTGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 120
DB 87 ATCAGGCTCTACTTCATAGTCTTATTGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 146

QY 121 CTCCTGGTGAANAATGAACCCCGGTGACGACCAATGCGGTGCTAATTAATCTGGTGGTG 180
DB 147 CTCCTGGTGAANAATGAACCCCGGTGACGACCAATGCGGTGCTAATTAATCTGGTGGTG 206

QY 181 GTCCACAGCGTTTTCGTGTCAGAGTGCATTTGCTTGGCTTACCTACCTCATCAAGAGACT 240
DB 207 GTCCACAGCGTTTTCGTGTCAGAGTGCATTTGCTTGGCTTACCTACCTCATCAAGAGACT 266

QY 241 TGGATGTTGGGCTGCCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
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Db	361	AAAGCAAGTGGAAATCTACAGAAACTGCATGCTGGCTGCCAGTGGCATGTGG	420
Qy	421	ACGCTGGTGAATGTCATGTTGGTACCCCTGGTGTCTCCCGGTATGGATCCATCAGGAA	480
Db	421	ACGCTGGTGAATGTCATGTTGGTACCCCTGGTGTCTCCCGGTATGGATCCATCAGGAA	480
Qy	481	TACATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGTGAATC	540
Db	481	TACATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGTGAATC	540
Qy	541	ATCAACTATATAGTACATTTTGTATAGCCGTGTGTGATCTGTGCTTCCAG	600
Db	541	ATCAACTATATAGTACATTTTGTATAGCCGTGTGTGATCTGTGCTTCCAG	600
Qy	601	GTCTTCATCATATGTTGATGTCAGAGCTAGCCACTCTTTACTATCCACAGGAG	660
Db	601	GTCTTCATCATATGTTGATGTCAGAGCTAGCCACTCTTTACTATCCACAGGAG	660
Qy	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTTGTCTTCCC	720
Db	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTTGTCTTCCC	720
Qy	721	TACAGTCTTTAGGATCTATTTGATGTGTGACGCAATCCAAATGCCCTGTAAACAGC	780
Db	721	TACAGTCTTTAGGATCTATTTGATGTGTGACGCAATCCAAATGCCCTGTAAACAGC	780
Qy	781	AAGGTTGCAATTTTAAACGAATCTTTCTGAGTGTAAAGCAATAGCTGTATGATTG	840
Db	781	AAGGTTGCAATTTTAAACGAATCTTTCTGAGTGTAAAGCAATAGCTGTATGATTG	840
Qy	841	CTTCTCTTTGCTTTGGGGAGAGCCATTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT	900
Db	841	CTTCTCTTTGCTTTGGGGAGAGCCATTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT	900
Qy	901	TGTGTTTGTGCGCGTTAG 918	
Db	901	TGTGTTTGTGCGCGTTAG 918	

RESULT 6

US-10-293-171-1

Sequence 1, Application US/10293171

Publication No. US20030138418A1

GENERAL INFORMATION:

APPLICANT: Eishengdrel, Haifeng

APPLICANT: Cai, Jidong

APPLICANT: Gassenhuber, Johann

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH

FILE REFERENCE: USA2001/0158 US NP

CURRENT APPLICATION NUMBER: US/10/293,171

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1040

TYPE: DNA

ORGANISM: homo sapiens

US-10-293-171-1

Query Match

Best Local Similarity

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 918; DB 15; Length 1040;

100.0%; Pred. No. 3e-270;

Qy	1	ATGCTGGCCACATACCTCCAGGAATTCCTCTGGGATCCCTATAGTGACACCCCACTTA	60
Db	1	ATGCTGGCCACATACCTCCAGGAATTCCTCTGGGATCCCTATAGTGACACCCCACTTA	60
Qy	61	ATCAGCCTCTACTTCATAGTGTCTTATGGGGCTGGTGGGTGTCTATTTCCATCTTTTC	120
Db	61	ATCAGCCTCTACTTCATAGTGTCTTATGGGGCTGGTGGGTGTCTATTTCCATCTTTTC	120

Qy	121	CTCCTGTTGAAATGAACACACCGGTGAGTGACCAACCATGCGGTCAATTAACTTGGTGGT	180
Db	121	CTCCTGTTGAAATGAACACACCGGTGAGTGACCAACCATGCGGTCAATTAACTTGGTGGT	180
Qy	181	GTCCACAGCGTCTTCTGCTGACAGTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
Db	181	GTCCACAGCGTCTTCTGCTGACAGTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
Qy	241	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGGCATGTGTCACATCCACATGTAC	300
Db	241	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGGCATGTGTCACATCCACATGTAC	300
Qy	301	CTCAGTTCCTATTTCTATGTTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Db	301	CTCAGTTCCTATTTCTATGTTGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Qy	361	AAAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGCTGCCAGTGTGCTGCCATGTGG	420
Db	361	AAAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGCTGCCAGTGTGCTGCCATGTGG	420
Qy	421	ACGCTGGTGAATCTCATTTGTTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Db	421	ACGCTGGTGAATCTCATTTGTTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Qy	481	TACATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAATC	540
Db	481	TACATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAATC	540
Qy	541	ATCAACTATATGATAGTCAATTTTGTATAGCCGTGTGTGATCTGTGTTGCTTCCAG	600
Db	541	ATCAACTATATGATAGTCAATTTTGTATAGCCGTGTGTGATCTGTGTTGCTTCCAG	600
Qy	601	GTCTTCATCATATGTTGATGTCAGAGCTAGCCACTCTTTACTATCCACAGGAG	660
Db	601	GTCTTCATCATATGTTGATGTCAGAGCTAGCCACTCTTTACTATCCACAGGAG	660
Qy	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCCC	720
Db	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCCC	720
Qy	721	TACAGTCTTTAGGATCTATTTGATGTGTGACGCAATCCAAATGCCCTGTAAACAGC	780
Db	721	TACAGTCTTTAGGATCTATTTGATGTGTGACGCAATCCAAATGCCCTGTAAACAGC	780
Qy	781	AAGGTTGCAATTTTAAACGAATCTTTCTGAGTGTAAAGCAATAGCTGTATGATTG	840
Db	781	AAGGTTGCAATTTTAAACGAATCTTTCTGAGTGTAAAGCAATAGCTGTATGATTG	840
Qy	841	CTTCTCTTTGCTTTGGGGAGAGCCATTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT	900
Db	841	CTTCTCTTTGCTTTGGGGAGAGCCATTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT	900
Qy	901	TGTGTTTGTGCGCGTTAG 918	
Db	901	TGTGTTTGTGCGCGTTAG 918	

RESULT 7

US-10-017-161-1193

Sequence 1193, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKINO

APPLICANT: ASAI, KIYOSHI

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084395/0152

CURRENT APPLICATION NUMBER: US/10/017,161

PRIOR FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR FILING DATE: 2001-06-18

US-10-017-161-1193

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; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Harland, Lee
; APPLICANT: Pfizer Inc.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10970AGLX
; CURRENT APPLICATION NUMBER: US/10/055,106C
; PRIOR FILING DATE: 2002-01-23
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-055-106c-1

Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGGCTCTACTTATAGTGCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTC 120
DB 61 ATCAGGCTCTACTTATAGTGCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTC 120
QY 121 CTCTGGTGAATAGAACACCCGGTGTGACACCAATGCGGTCTATTAACCTGGTGGTG 180
DB 121 CTCTGGTGAATAGAACACCCGGTGTGACACCAATGCGGTCTATTAACCTGGTGGTG 180
QY 181 GTCCACAGCGTTTCTGTGTGACAGTGCCTATTTGGTGTGACCTCATCAAGAGACT 240
DB 181 GTCCACAGCGTTTCTGTGTGACAGTGCCTATTTGGTGTGACCTCATCAAGAGACT 240
QY 241 TGGATGTTGGGCTGCCCCCTTCTGCAAAATTTGTGAGTGCCATGTGACATCCCATGTAC 300
DB 241 TGGATGTTGGGCTGCCCCCTTCTGCAAAATTTGTGAGTGCCATGTGACATCCCATGTAC 300
QY 301 CTCACGTTCTATTTCTATGTGGTGATCTCTGTCACAGATPACCTCATCTTCTCAAGTGC 360
DB 301 CTCACGTTCTATTTCTATGTGGTGATCTCTGTCACAGATPACCTCATCTTCTCAAGTGC 360
QY 361 AAAGACAAAGTGAATTTCTACAGAAACTGCTGTGGCTGCCAGTGTGCGCATGTGG 420
DB 361 AAAGACAAAGTGAATTTCTACAGAAACTGCTGTGGCTGCCAGTGTGCGCATGTGG 420
QY 421 ACCTGGTGATTTGTCATTTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 ACCTGGTGATTTGTCATTTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 TACAATGAGGAGCAGCTGTTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
DB 481 TACAATGAGGAGCAGCTGTTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
QY 541 ATCAACTATATAGTATGATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 ATCAACTATATAGTATGATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCTTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 660
DB 601 GTCTTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 660
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTGATCTTGTGTTGTTTCTTCC 720
DB 661 TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTGATCTTGTGTTGTTTCTTCC 720

RESULT 5
US-10-188-405-9
; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cusler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1e1 Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR343
; US-10-188-405-9

Query Match 100.0%; Score 918; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGGCTCTACTTATAGTGCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTC 120
DB 61 ATCAGGCTCTACTTATAGTGCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTC 120
QY 121 CTCCTGGTGAATAGAACACCCGGTGTGACACCAATGCGGTCTATTAACCTGGTGGTG 180
DB 121 CTCCTGGTGAATAGAACACCCGGTGTGACACCAATGCGGTCTATTAACCTGGTGGTG 180
QY 181 GTCCACAGCGTTTCTGTGTGACAGTGCCTATTTGGTGTGACCTCATCAAGAGACT 240
DB 181 GTCCACAGCGTTTCTGTGTGACAGTGCCTATTTGGTGTGACCTCATCAAGAGACT 240
QY 241 TGGATGTTGGGCTGCCCCCTTCTGCAAAATTTGTGAGTGCCATGTGACATCCCATGTAC 300
DB 241 TGGATGTTGGGCTGCCCCCTTCTGCAAAATTTGTGAGTGCCATGTGACATCCCATGTAC 300
QY 301 CTCACGTTCTATTTCTATGTGGTGATCTCTGTCACAGATPACCTCATCTTCTCAAGTGC 360
DB 301 CTCACGTTCTATTTCTATGTGGTGATCTCTGTCACAGATPACCTCATCTTCTCAAGTGC 360
QY 361 AAAGACAAAGTGAATTTCTACAGAAACTGCTGTGGCTGCCAGTGTGCGCATGTGG 420
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;; PRIOR APPLICATION NUMBER: 60/309,208  
;; PRIOR FILING DATE: 2001-07-31  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 918  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-995-225-3

Query Match 100.0%; Score 918; DB 9; Length 918;  
Best Local Similarity 100.0%; Pred. No. 2.8e-270;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60  
DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTCATAGTGCCTTATTGGGGGCTGGTGGTGTCTATTCATTCCTTTTC 120  
DB 61 ATCAGCCTCTACTTCATAGTGCCTTATTGGGGGCTGGTGGTGTCTATTCATTCCTTTTC 120

QY 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGGCGGTCACTTAACCTTGGTGGTG 180  
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGGCGGTCACTTAACCTTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTCTGCTGACAGTGCCTTGGCTTGGCTGACCTCATCAAGAGACT 240  
DB 181 GTCCACAGCGTTTCTCTGCTGACAGTGCCTTGGCTTGGCTGACCTCATCAAGAGACT 240

## RESULT 2

US-09-995-225-3  
; Sequence 3, Application US/09995225  
; Publication No. US20030139588A9

## GENERAL INFORMATION:

;; APPLICANT: Chen, Ruoping

;; APPLICANT: Chu, Zhi Liang

;; APPLICANT: Dang, Huang T.

;; APPLICANT: Lowitz, Kevin P.

;; APPLICANT: Pridie, Cameron

;; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G

;; FILE OF INVENTION: Receptors

;; FILE REFERENCE: AREN-0308

;; CURRENT APPLICATION NUMBER: US/09/995,225

;; CURRENT FILING DATE: 2001-11-26

;; PRIOR APPLICATION NUMBER: 60/170,496

;; PRIOR FILING DATE: 1998-10-13

;; PRIOR APPLICATION NUMBER: PCT/US99/23938

;; PRIOR FILING DATE: 1998-10-13

;; PRIOR APPLICATION NUMBER: 60/253,404

;; PRIOR FILING DATE: 2000-11-27

;; PRIOR APPLICATION NUMBER: 60/255,366

;; PRIOR FILING DATE: 2000-12-12

;; PRIOR APPLICATION NUMBER: 60/270,286

;; PRIOR FILING DATE: 2001-02-20

;; PRIOR APPLICATION NUMBER: 60/282,032

;; PRIOR FILING DATE: 2001-04-06

;; PRIOR APPLICATION NUMBER: 60/282,358

;; PRIOR FILING DATE: 2001-04-06

;; PRIOR APPLICATION NUMBER: 60/282,356

;; PRIOR FILING DATE: 2001-04-06

;; PRIOR APPLICATION NUMBER: 60/290,917

;; PRIOR FILING DATE: 2001-05-14

;; PRIOR APPLICATION NUMBER: 60/309,208

;; PRIOR FILING DATE: 2001-07-31

;; NUMBER OF SEQ ID NOS: 67

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 3

;; LENGTH: 918

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-09-995-225-3

Query Match 100.0%; Score 918; DB 10; Length 918;  
Best Local Similarity 100.0%; Pred. No. 2.8e-270;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60  
DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTCATAGTGCCTTATTGGGGGCTGGTGGTGTCTATTCATTCCTTTTC 120  
DB 61 ATCAGCCTCTACTTCATAGTGCCTTATTGGGGGCTGGTGGTGTCTATTCATTCCTTTTC 120

QY 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGGCGGTCACTTAACCTTGGTGGTG 180  
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACCATGGCGGTCACTTAACCTTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTCTGCTGACAGTGCCTTGGCTTGGCTGACCTCATCAAGAGACT 240  
DB 181 GTCCACAGCGTTTCTCTGCTGACAGTGCCTTGGCTTGGCTGACCTCATCAAGAGACT 240



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:41:59 ; Search time 460 Seconds  
(without alignments)  
8997.651 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgctgcccacatacctc.....attgtgttttgcggttag 918

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications NA.\*

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- 2: /cgn2\_6/ptodata/2/pubnpna/US07\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubnpna/US06\_PUBCOMB.seq.\*
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- 19: /cgn2\_6/ptodata/2/pubnpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	918	100.0	918	9	US-09-995-225-3	Sequence 3, Appli
2	918	100.0	918	10	US-09-995-225-3	Sequence 3, Appli
3	918	100.0	918	13	US-10-297-908A-2	Sequence 2, Appli
4	918	100.0	918	13	US-10-055-106C-1	Sequence 9, Appli
5	918	100.0	918	15	US-10-188-405-9	Sequence 1, Appli
6	918	100.0	1040	15	US-10-293-171-1	Sequence 1, Appli
7	918	100.0	1318	15	US-10-017-161-1193	Sequence 1193, Ap
8	918	100.0	2525	10	US-09-782-974C-81	Sequence 81, Appl
9	918	100.0	113306	16	US-10-292-798A-81	Sequence 1007, Ap
10	916.4	99.8	1684	15	US-10-085-233B-1	Sequence 1, Appli
11	913.4	99.5	939	15	US-10-085-233B-3	Sequence 3, Appli
12	560.8	61.1	810	15	US-10-366-504-1	Sequence 1, Appli
13	390	42.5	447	10	US-09-782-974C-21	Sequence 21, Appl
14	76.4	8.3	1113	11	US-09-826-509-540	Sequence 540, App

ALIGNMENTS

RESULT 1

US-09-995-225-3  
; Sequence 3, Application US/0995225  
; Publication No. US20020193584A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Chu, Zhi Liang  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Priddy, Cameron  
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
; FILE REFERENCE: AREN-0308  
; CURRENT APPLICATION NUMBER: US/09/995,225  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/253,404  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/255,366  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/270,286  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,365  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/270,266  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/282,032  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,358  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/282,356  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/290,917  
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61 6.6 1143 11 US-09-826-509-542  
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61 6.6 1182 15 US-10-225-567A-147  
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58 6.3 1002 15 US-10-251-385-15  
58 6.3 1002 15 US-10-251-385-171  
58 6.3 1002 15 US-10-225-567A-278  
58 6.3 1023 13 US-10-433-561-12  
58 6.3 1518 15 US-10-305-720-1480

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Sequence 208, App  
Sequence 31, Appli  
Sequence 7, Appli  
Sequence 8, Appli  
Sequence 1345, Ap  
Sequence 9800, Ap  
Sequence 1, Appli  
Sequence 23500, A  
Sequence 9, Appli  
Sequence 542, App  
Sequence 21, Appli  
Sequence 147, App  
Sequence 19, Appli  
Sequence 1417, Ap  
Sequence 19, Appli  
Sequence 14, Appli  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 15, Appli  
Sequence 171, App  
Sequence 278, App  
Sequence 12, Appli  
Sequence 1480, Ap

assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

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Location/Qualifiers  
/organism="Mus musculus"  
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QY 121 CTCCTGGTGAATGAACACCCCGTCAGTG 150  
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DEFINITION  
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ACCESSION  
CD469227.1 GI:31390495  
VERSION  
EST.  
SOURCE  
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ORGANISM  
Equus caballus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
REFERENCE  
1 (bases 1 to 679)  
Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,  
Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.  
An EST database from equine (Equus caballus) stimulated peripheral  
blood leukocytes  
Unpublished (2003)  
Other ESTs: LeukoS2\_2\_H07.bl.A024  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; tissue and RNA were prepared in the Department of Large  
Animal Medicine, University of Georgia; sequencing done in the  
Laboratory for Genomics and Bioinformatics, University of Georgia.  
Sequence ends have been trimmed to exclude vector and regions below  
phred quality 16. Three-prime sequences are presented as their  
reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).

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isolated from a healthy adult horse. The leukocytes were  
stimulated for 4 hr with 10 ng/ml E. coli O55:85 LPS.  
Double-stranded cDNA was cloned unidirectionally into  
different DraIII sites of the pME18S-FL3 vector (5-prime  
DraIII site is CACTGTGTG, 3-prime DraIII site is  
CACCATGTG). XhoI excises the cDNA insert."

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Query Match 8.5%; Score 77.8; DB 14; Length 679;  
Best Local Similarity 49.9%; Pred. No. 5.4e-10;  
Matches 255; Conservative 0; Mismatches 247; Indels 9; Gaps 2;  
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QY 538 ATCATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597  
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QY 658 GAGTTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGATCTCTTTGTTTCTTTTCTTT 717  
Db 335 GAGTATAGAGCTCAAAATCAAGAGCTGCTTCTTCTCTAGTAATAGTCGCTCTGTTTATA 394  
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Db 395 CCCACCATGATTCGGGTACACT-----TCTTCAGATTTATTCAGAGGGAGAAAAT 448  
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Qy 188 GCGTTTTT-CGTGTCAGAGTGCATTTGCTGTGACC---TACCTCATCAAGAGACTGG 243
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dendritic cells Mus musculus cDNA clone F630103H01 5', mRNA
sequence.
ACCESSION BY748361
VERSION BY748361.1 GI:27177122
KEYWORDS EST.
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SOURCE  
ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.REFERENCE  
AUTHORS

1 (bases 1 to 661)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Shionobach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,  
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,  
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,  
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,  
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,  
Maltais, D., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, I.,  
Wells, C., Wilming, L. G., Wysshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, K., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

JOURNAL  
MEDLINE  
PUBMED

22354683

## COMMENT

Contact: Yoshihide Hayaehizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
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Fax: 81-45-503-9216  
Email: genome.res@sc.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nomura, K., Numazaki, R., Ohno, M., Osato, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
Takeda, Y., Waki, K., Watanabe, M., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC building Addenbrookes Hospital Cambridge) whose

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DEFINITION	627748 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT8K09_A_F05 5', mRNA sequence.
ACCESSION	CA355790
VERSION	CA355790.1 GI:24600977
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SOURCE	Oncorhynchus mykiss (rainbow trout)
ORGANISM	Oncorhynchus mykiss
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
AUTHORS	1 (bases 1 to 680)
TITLE	Rexroad, C.E. and Keele, J.W.
JOURNAL	Sequence analysis of a rainbow trout normalized cDNA library
COMMENT	Unpublished (2002) Contact: Rexroad CE USDA, ARS, National Center for Cool and Cold Water Aquaculture 11876 Lestown Road, Kearneysville, WV 25430, USA Tel: 304 724 8340 x2129 Fax: 304 725 0351 Email: crexroad@nccwa.ars.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329. Seq primer: AGCGGATAACAATTTCACACGGA. Location/Qualifiers 1. .680 /organism="Oncorhynchus mykiss" /mol_type="mRNA" /db_xref="taxon:8022" /clone="1RT8K09_A_F05" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="NCCWA 1RT" /note="Vector: pCMV SPORt6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
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DB	425 CTGCTGTTACTGGATGTTGGGGAGATGCTGTGTAAGNGGTGAGTGCATGATCCACG 484
QY	290 TCCATGATGATCACTCAGTTCCTCTATTTATGTTGGTATCTGTTGCCAGATACCTCATCT 349
DB	485 TGCATGATGATGCTTTTGTCTTCTACGTGGTCACTCCTCGTCTCATACGACTGCTGGGGT 544
QY	350 TCTTCAAGTGCAGAGACAAAGTGGAAATTTACAGAAAACATGCTGTGGCTGCCAGTG 409
DB	545 TCCATAGCAAGAGATCGCTACAGTTCTACAGAAAGTTCATGCTTTTGGCGCCAGTG 604
QY	410 CTGGCAGTGGACGCTGGTGTATGTCATTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 469
DB	605 TGGCAGTGTGACAGTGTATGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 664
QY	470 TCCATGAGGATACAA 485
DB	665 AGGACGTCACGATAA 680
RESULT 13	
LOCUS	CA965628 844 bp mRNA linear EST 03-JAN-2003
DEFINITION	CCLX05a15h17f1 Carp mixed tissue library 2 Cyprinus carpio cDNA clone 15h17 5', mRNA sequence.
ACCESSION	CA965628
VERSION	CA965628.1 GI:27492185
KEYWORDS	EST.
SOURCE	Cyprinus carpio (common carp)
ORGANISM	Cyprinus carpio
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.
AUTHORS	1 (bases 1 to 844)
TITLE	Gracey, A.Y., Fraser, E., Li, W. and Cossins, A.R.
JOURNAL	Microarray and EST analysis of the carp (Cyprinus carpio) transcriptome during environmental stress
COMMENT	Unpublished (2003) Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST. Plate: 15 row: h column: 17 Seq primer: TripleX 5' LD (5'-CTCGGAAGCGCCCATTTGTTGGT-3') High quality sequence start: 39 High quality sequence stop: 580. Location/Qualifiers 1. .844 /organism="Cyprinus carpio" /mol_type="mRNA" /db_xref="taxon:7962" /clone="15h17" /sex="Male & female"
FEATURES	source

## AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, K., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

## TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>  
URL: <http://fantom.gsc.riken.go.jp/>

## FEATURES

Location/Qualifiers  
1..2774  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM\_DB:A530099J19"  
/db\_xref="MGI:2406345"  
/db\_xref="taxon:10090"  
/clone="A530099J19"  
/sex="male"  
/tissue\_type="aorta and vein"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
311..1210  
CDS  
/note="unnamed protein product; hypothetical  
Rhodopsin-like GPCR superfamily containing protein  
(InterPro|IPR000276, evidence: InterPro)  
putative"  
/codon\_start=1  
/protein\_id="BAC30904.1"  
/db\_xref="GI:26334373"  
/translation="MDVMDVLSNGSVMPMAEQVCDACRAILTYAVSVFFGFT  
VGTVMHMFRRKQSMIATIIINIIIVLSLLISLPRLSYFSAVKLGSPFCRM  
VGVIVGHMYLTFIPYVAIVTLRIIVFKLQMOLOKFAVALSIITVWTSRIFLP  
IFPLQYGDPSYTSQRCFEPHKSINRDIINYSIIVIMVTLLFLIQAVILH  
LIKAYWDMWAHQRYRAIKSPFLLIVVCFIHPHAFRVYFIQNPPEQENSKLILYN  
EICVALTAFCLDMELCTFGVVIH"

## CDS

## RESULT 11

AJ455645  
LOCUS  
AJ455645 riken1 Gallus gallus CDNA clone 6b4r1, mRNA linear EST 22-APR-2002  
DEFINITION  
AJ455645  
ACCESSION  
AJ455645.1 GI:20265741  
VERSION  
AJ455645.1  
KEYWORDS  
EST.  
SOURCE  
Gallus gallus (chicken)  
ORGANISM  
Gallus gallus  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

1 (bases 1 to 834)  
Buerstedde, J.M.  
Gallus gallus bursal lymphocyte EST  
Unpublished (2002)  
Contact: Buerstedde JM  
Cellular Immunology  
Heinrich-Pette-Institute  
Martinistr. 52, 20251 Hamburg, Germany  
Email: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.  
Location/Qualifiers  
1..834  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="6b4r1"  
/cell\_type="bursal lymphocyte"

## FEATURES

source

1..834

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="6b4r1"

/cell\_type="bursal lymphocyte"

## ORIGIN

Query Match 15.9%; Score 146.2; DB 11; Length 2774;  
Best Local Similarity 51.7%; Pred. No. 1.7e-28;  
Matches 412; Conservative 0; Mismatches 373; Indels 12; Gaps 3;  
77 TAGTCTATTGGCGGCTGGTGGTGCATTCATTCATTCCTCTCTCTGTAATGA 136  
423 TGGTCTCTTTGGAGGCACCGGTGGAAACAGTATGATGTCACATGATGTTCAAGAGGA 482  
137 ACACCCGCTAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGTGGTCCACACGCGTTTTC 196  
483 ATTGCCATCATGATTGCCACTATCATCATTAATATCATTTGTTGCACTCCCTTCTCC 542  
197 TGCTGACAGTGCCATTTCGTTGACCTACCTCATCAAGAACATTTGGATGTTGGGCTGC 256  
543 TGAATTAGTCTGCCATTCCGCTCTCAGTTACTATTTCTCAGCAGTCTGGAAGCTGGTCTT 602

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTTACCACTCAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Betrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Patima Bonaldo."

## ORIGIN

Query Match 16.5%; Score 151.4; DB 12; Length 478;  
Best Local Similarity 81.7%; Pred. No. 3.1e-30;  
Matches 187; Conservative 0; Mismatches 41; Indels 1; Gaps 1;  
QY 690 TATAGGGGTCATCTGTTTGTTCCTCCCTACACAGGTTGCATTATATACGGAATCTTCT 809  
DB 1 TATAGGTCATCATTTATTATTTGTTT-CTTCCTACCAAGTCTTTCAGGATTATTTACTTGTA 59  
QY 750 TGTGTGACCCATCCATCCCTGCTACACAGGTTGCATTATATACGGAATCTTCTT 809  
DB 60 TGTGTGGCATTCCCAAGAGCTGTAAACAAGTTCATTATACATGAATCTTAT 119  
QY 810 GAGTGTAAACAGCAATATGCTGATGATTTGCTTCTTTGCTTTTGGGGAGCCATTG 869  
DB 120 GAGCACACAGCCATCAGCTGCTGTGATTTGCTGCTTTTGTCTTTGGAGGAGCCATTG 179  
QY 870 GTTTACCAAGTAATTCGCTATGGAATGTTGTTTGGCGGTAG 918  
DB 180 GGTTAGCAAAAGATTGCACATGTGGAATTCCTCTTAAGCCATTAG 228

## RESULT 9

BG221739 283 bp mRNA linear EST 21-APR-2001  
LOCUS BG221739  
DEFINITION R641554 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG221739  
VERSION BG221739.1 GI:13747760  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1 (bases 1 to 283)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,  
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,  
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,  
Offenbacher, J., Danzig, J., and Ducar, M.

Creation of genome-wide protein expression libraries using random

## TITLE

activation of gene expression

## JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

## MEDLINE

21227151

## PUBMED

11329013

## COMMENT

Contact: Scott J. Cain

Athersys, Inc. Cleveland, OH 44115, USA

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 233.

Location/Qualifiers

## FEATURES

1..283  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="HT1080"  
/clone\_lib="Athersys RAGE Library"  
/notes="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 16.1%; Score 148; DB 12; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.1e-29;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCCAATACCTCCAGGAATCTCTTCGATCTATAGTGACACCCACTTA 60  
DB 136 ATGCTGGCCCAATACCTCCAGGAATCTCTTCGATCTATAGTGACACCCACTTA 195

QY 61 ATCAGCCTTACTTCACTAGTCTTATTGGCGGGCTGGTGGTGTCAATTCATTTCTTTTC 120  
DB 196 ATCAGCCTTACTTCACTAGTCTTATTGGCGGGCTGGTGGTGTCAATTCATTTCTTTTC 255

QY 121 CTCCTGGTGAATAATGACACCCGCTCAG 148

DB 256 CTCCTGGTGAATAATGACACCCGCTCAG 283

## RESULT 10

## AK041317

## LOCUS

## DEFINITION

Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A53009J19 product:hypothetical Rhodopsin-like GPCR superfamily containing protein, full insert sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

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## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match      20.6%; Score 189; DB 14; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGGACAAATACCTCCAGCAATTCCTCTTGCGATCCCTATAGTGACACCCACTTA 60
DB 311 ATGCTGGGACAAATACCTCCAGCAATTCCTCTTGCGATCCCTATAGTGACACCCACTTA 370
QY 61 ATCAGCCTCTACTTCATAGTCTTATGCGGCTGGTGGGTCTCATTTCCATTTCTTC 120
DB 371 ATCAGCCTCTACTTCATAGTCTTATGCGGCTGGTGGGTCTCATTTCCATTTCTTC 430
QY 121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGGTCAATTAACCTGGTGG 180
DB 431 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGGTCAATTAACCTGGTGG 490
QY 181 GTCCACAGC 189
DB 491 GTCCACAGC 499

RESULT 7
BG461295
LOCUS
DEFINITION
RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG461295
VERSION
BG461295.1 GI:13749801
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 649)
AUTHORS
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE
Activation of genome-wide protein expression libraries using random
creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL
Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE
21227151
PUBMED
11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaineatersys.com.
FEATURES
source
1..649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match      19.3%; Score 176.8; DB 12; Length 649;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGGACAAATACCTCCAGCAATTCCTCTTGCGATCCCTATAGTGACACCCACTTA 60
DB 311 ATGCTGGGACAAATACCTCCAGCAATTCCTCTTGCGATCCCTATAGTGACACCCACTTA 370
QY 61 ATCAGCCTCTACTTCATAGTCTTATGCGGCTGGTGGGTCTCATTTCCATTTCTTC 120
DB 371 ATCAGCCTCTACTTCATAGTCTTATGCGGCTGGTGGGTCTCATTTCCATTTCTTC 430
QY 121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGGTCAATTAACCTGGTGG 180
DB 431 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGGTCAATTAACCTGGTGG 490
QY 181 GTCCACAGC 189
DB 491 GTCCACAGC 499
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Best Local Similarity 75.5%; Pred. No. 3.8e-37;
Matches 323; Conservative 0; Mismatches 47; Indels 58; Gaps 6;

QY 38 ATCTATAGTGACACCCACCTTAATCAGCCCTCTACTTCTATAGTCTTATTTGGCGGCTGG 97
DB 143 ATCTATAGTGACACCCACCTTAATCAGCCCTCTACTTCTATAGTCTTATTTGGCGGCTGG 202
QY 98 TGGGTGTCATTTCCATTTCTTTCTCTCTGTTGAAATGAACACCCGGTCACTGACACCA 157
DB 203 AGGGTGTCTATTTCCATTTCTTTCTCTCTGTTGAAATGAACACCCGGTCACTGACACCA 245
QY 158 TGGCGGTCTATTAACCTTGCTGGTGTGCACACGCTTTTCTGTCACAGTG-CCATTTTCG 216
DB 246 TGGCGGTCTATTAACCTTGCTGGTGTGCACACGCTTTTCTGTCACAGTG-CCATTTTCG 305
QY 217 TTGACCTACCTCATCAAGAGACTTGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGT 276
DB 306 TTGACCTACCTCAAGAGACTTGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGT 347
QY 277 GCCATGTGACATCCACATGCTACCTCAGCTTCTCT-ATTCTATGTTGATCTGCTGTCAC 335
DB 348 ACCATGCTCAACATTCATGCTACCTGACGATCTCTAAATTTCTATGGCGTGTATCTCGGCC 407
QY 336 CAGATACCTCATCTTCTTCAAGTGCACAAAGACAAAGTGGAAATTTACAGAAAACCTGCATGC 395
DB 408 CGGAT-----CAAGACAAAGCGACTT-TACAGAGTGTCTGGCCCC 446
QY 396 TGTGGCTGCCAGTCTGCGATGTCGACGCTGGTGAATTTCTATGTTGATGCCCTGTTGT 455
DB 447 CGAGGTTGCCAGAGCTGGCATGTGGACCTGTTGATTTGATTTGTTACTCGCGCCCCCGCGTGT 506
QY 456 CTCGCCGT 463
DB 507 TTCGCCGT 514

RESULT 8
BG145683
LOCUS
DEFINITION
mac33c07.Y1 Soares mouse 3NDMS Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.
ACCESSION
BG145683
VERSION
BG145683.1 GI:12649019
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 478)
AUTHORS
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1499380
Seq primer: -40RP from Gibco
High quality sequence stop: 392.
FEATURES
source
1..478
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4001652"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse 3NDMS"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
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Db      480  GCTGTTGCGTTCATCTCTGTTGGTTCCAGGTCCTTCATCACATGTCCTCCATGGCGGAG 539
Qy      631  CTACGCCACTCTTTACTATCCACACAGAGTCTCTGGCTCAGCTGAAACCTATTTT 690
Db      540  TTTGCGCACTCTTACTAT-CCACACAGAGTCTCTGGCACTGAAACCTATTTT 598
Qy      691  ATAGGGGTCA---TCTGTTGTTTCTTCCCTACCACTCTTTAGGATCTTACTTTG 747
Db      599  ATAGGTATCACTATCCATTTGGTTCTTCCCTACCACTCTTCCAGAT-TATTACTGT 657
Qy      748  AATGTTGTGACCACTTCCAAATCCCTGTAA 776
Db      658  TGTGTTGGGGCGTCCCAAGCTGGTA 686

RESULT 3
LOCUS   AZ554824
DEFINITION RPCI-23-211E13.TV RPCI-23 Mus musculus genomic clone
ACCESSION AZ554824
VERSION   AZ554824.1 GI:11234644
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 580)
AUTHORS   Zhao,S., Nierman,W., Feidblyum,T., Malek,J., Shatman,S.,
          Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
          Jong,P. and Fraser,C.M.
          Mouse BAC End Sequences from Library RPCI-23
          Unpublished (1999)
          Other_GSSs: RPCI-23-211E13.TU
          Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@cigr.org
          Clones are derived from the mouse BAC library RPCI-23. For BAC
          library availability, please contact Pieter de Jong
          (pieter@dejong.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
          or from Resea ch Genetics (info@resgen.com). BAC end page:
          http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
          Plate: 211 row: E column: 13
          Seq primer: 17
          Class: BAC ends.
          Location/Qualifiers
            1..580
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              /mol_type="genomic DNA"
              /strain="CS7BL/6J"
              /db_xref="taxon:10090"
              /clone="RPCI-23-211E13"
              /sex="Female"
              /lab_host="DH10B"
              /clone_lib="RPCI-23"
              /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
              EcoRI; Site_2: EcoRI; Female CS7BL/6J mouse kidney and/or
              brain genomic DNA was isolated and partially digested
              with a combination of EcoRI and EcoRI Methyase. Size
              selected DNA was cloned into the pBACe3.6 vector at the
              EcoRI sites. The ligation products were transformed into
              DH10B electrocompetent cells (BRL Life Technologies)."
```

## ORIGIN

```

Query Match      38.3%; Score 351.4; DB 28; Length 580;
Best Local Similarity 79.9%; Pred. No. 5e-85;
Matches 426; Conservative 0; Mismatches 106; Indels 1; Gaps 1;
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```

Qy      386  AACTGCATGCTGTGGTCCAGTCTGGCATGTGGAGCGTGGTCAATGTGATGTGGTAC 445
Db      1    AATTGCATGAGTTGCTGCAAGTTCT-GCCTGTGGCTTCTGGTATTGTTGTTGTC 59
Qy      446  CCCTGGTTGCTCCCGTATGGAATCCATGAGNAATCAATGAGGACATGTTTAAAT 505
Db      60    CCTTGGTGGTTCTCAGTATGGAATAGCGAAGAAATACAAATGAGCAACAGTCTTAGAT 119
Qy      506  TTCACAAAGAGCTTGTCTTACACATATGTGAAATCATCAACTATATGATAGTCAATTTTG 565
Db      120  TCCATAAAGAACTTGGCCATGATTCTGTGGAGTTATCAACTATATGATAGTCAATTTTG 179
Qy      566  TCATAGCCGTTGCTGTAATTCGTGTGCTCTTCAGGTCCTTCATCATATGATGATGTGTC 625
Db      180  TCATAGCTGTGGCTTGAATTCCTTGGGTTTCCAGGTCCTTCATCACATTCATGATGTC 239
Qy      626  AGAAGCTACGCCACTCTTTACTATCCACAGAGATTCGGCTCAGCTCAAAAACCTAT 685
Db      240  GGAAGTTTCGCCACTCTTACTATCCACAGAGTTCTGGGCACAACTGAAAAATCTTT 299
Qy      686  TTTTATAGGGGTCACTCCTTGTGTTTCTTCCCTACCACTCTTTAGGATCTTACT 745
Db      300  TCCTTATAGGTATCATATTATTGTTTCTTCCCTACCACTCTTCCAGGATTTACT 359
Qy      746  TGAATGTTGTGAGCATTCCAAATGCCCTGTAACAGCAGGTTCATTTTATAACGAAATCT 805
Db      360  TGTATGTTGTGGACATTCACAGAGCTGTAAACAAAGTGCATTTTCAATGAAATCC 419
Qy      806  TCTTGAAGTAAACAGCAATTAGCTGTGATGATTTGCTCTCTTTGTTGGGGAGGCC 865
Db      420  TATTGAGCAACAACAGCCATCAGCTGCTGTGATTTGCTCTTTTGTCTTTGGAGAGGCC 479
Qy      866  ATTGGTTTAAAGCAAGATAATGGCTTATGGAATGTGTTTGTGCGCGTAG 918
Db      480  ATTGGGTTAAAGCAAGATTGTGACATGTGGAATTCCTCTTATGCCATTAG 532

RESULT 4
LOCUS   AQ888495
DEFINITION HS_3162_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey
          sequence.
ACCESSION AQ888495
VERSION   AQ888495.1 GI:6344685
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 456)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
          Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
          Hood,L.
          Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
          Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
          99380589
          PUBMED 10449764
          Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Clones may be purchased from Research Genetics (info@resgen.com).
          BAC end Web Server: http://www.htsc.washington.edu
          Plate: 3162 row: D column: 1
          Seq primer: M13 Reverse
          Class: BAC ends
          High quality sequence stop: 456.
          Location/Qualifiers
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## FEATURES

end was generated during the Red process and may have higher chance of clone tracking errors.

## PRIMERS

Sequencing: TJ

## LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. .684

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="Rp43-007G22.TJ"

/sex="male"

/cell\_type="lymphocytes"

/clone\_lib="RP43 Chimpanzee Male BAC Library"

## FEATURES

source

## ORIGIN

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Best Local Similarity 98.2%; Pred. No. 3e-137;  
Matches 548; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 10 AAAAAATCCGCGCTTCTACAGAAACTGCATGCTGGCTGCCAGTCTGGCATGTGG 69  
QY 421 ACCTGCTGATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAAATCCATGAGAA 480  
DB 70 ACCTGCTGATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAAATCCATGAGAA 129  
QY 481 TCAATGAGAGACACTGTTTAAATTCACAAAGACTGCTGTACATATGTGAAATC 540  
DB 130 TCAATGAGAGACACTGTTTAAATTCACAAAGACTGCTGTACATATGTGAAATC 189  
QY 541 ATCACTATATGATGATCAATTTTGTATAGCGGTTGCTGTGATTCGTGTTGCTTCCAG 600  
DB 190 ATCACTATATGATGATCAATTTTGTATAGCGGTTGCTGTGATTCGTGTTGCTTCCAG 249  
QY 601 GTCCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 250 GTCCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309  
QY 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720  
DB 310 TTCGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 369  
QY 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCCCTGTACACAGC 780  
DB 370 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCCCTGTACACAGC 429  
QY 781 AAGTTGCAATTTATACCAATCTTCTGAGTTAAGCAATGATGCTGATGATGATGATGATGATGAT 840  
DB 430 AAGTTGCAATTTATACCAATCTTCTGAGTTAAGCAATGATGCTGATGATGATGATGATGATGAT 489  
QY 841 CTTCTCTTTGCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATATTTGGCTTATGGAAT 900  
DB 490 CTTCTCTTTGCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATATTTGACATATGGAAT 549  
QY 901 TGTGTTTGTGCGGTAG 918  
DB 550 TGTGTTTGTGCGGTAG 567

## RESULT 2

## BF160725

## LOCUS

601769127F1 NCI\_CGAP\_Lu29 Mus musculus cdna clone IMAGE:3988230 5', 772 bp mRNA linear EST 30-OCT-2000

## DEFINITION

mRNA sequence.

## ACCESSION

BF160725

## VERSION

BF160725.1 GI:11040832

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 772)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cdna Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM9196 row: f column: 07

High quality sequence stop: 634.

## FEATURES

source

Location/Qualifiers

1. .772

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/mol\_type="mRNA"

/strain="Czech II"

/db\_xref="taxon:10090"

/clone="IMAGE:3988230"

/tissue\_type="spontaneous tumor, metastatic to mammary.

Stem cell origin."

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Lu29"

/note="Organ: lung; Vector: pCMV-Sport6; Site 1: Salt;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 45.3%; Score 416.2; DB 10; Length 772;  
Best Local Similarity 79.1%; Pred. No. 9.7e-103;  
Matches 545; Conservative 0; Mismatches 138; Indels 6; Gaps 4;

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DB 1 GGACTGTAGCGCTCATCTCCATCTCTTCTGCTGTGAAATGAACACTCACGTTCAAGT 60  
QY 151 ACCACCATGGCGGTCAATTAACCTGGTGGTGCACAGCGTTTCTCTGTCGACAGTCCCA 210  
DB 61 ACCACCATGGCTGCATCAACCTGGTGGTGCATGGGTCTTCTCTGACGGTGCCT 120  
QY 211 TTTGCTTGACCTACCTCATCAAGACAGCTTGAGATGTTGGGCTGCCCTTCTGCAAAATTT 270  
DB 121 TTCGGCTTGGCATACCTCATCAAGGACCTTGGACG-TTGGATTTACCTTCTGCAAAATTT 179  
QY 271 GTGAGTSCCATGCTGCACATCCATCTACTCAGCTTCTCTATTTCTATGTTGGTGCCTG 330  
DB 180 GTGAGTSCCATGTTACATATCCATGTTACTCATCTCTCTTCTACGTTGGTACTACTA 239  
QY 331 GTCACAGATACCTCATCTTCTTCAAGTGCAAGACAAAGTGAATTTCTACAGAAATCTG 390  
DB 240 GTCATCAGATACCTCATCTTCTTCAAGCGTAGACACAAAGTAGAATTTCTATAGAAATTTG 299  
QY 391 CATGCTGTGGTCCAGTGGTGGCATCTGGACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 450  
DB 300 CATGAGTGTGTCGAAGTCTGCCATCTGGCTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 359  
QY 451 GTTGTCTCCCGGTATGGAATCCATGAGGAATCAATGAGGAGCAGCTGTTTAAATTTTAC 510  
DB 360 GTGTTTCTCAGTATGGAATAGTGAAGATACATGAGCAACAGTCTTTAGATTCAT 419  
QY 511 AAAGAGCTTGTACATATGTGAAATCATCACTATATGATGATGATGATGATGATGATGATGAT 570  
DB 420 AAAGAGCTTGTGCAATGATCTGTGCGAGTTATCAACTACATGATGATGATGATGATGATGAT 479  
QY 571 GCGGTGTGCTGATTTCTGTTGGTCTTCCAGTCTTTCATCATTTATGTTGATGTTGTCAGAG 630

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:13:09 ; Search time 2947 Seconds  
(without alignments)

9302.166 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgctggccacaataacctc.....attgtgtttgtgcgcttag 918

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmvi.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rtd.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_ges1.\*  
29: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	542	59.0	684	29	AG145972 Pan trogl
2	416.2	45.3	772	10	BF160725 601769127
3	351.4	38.3	580	28	AZ554824 RPCI-23-2
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6	189	20.6	499	14	CD699779
7	176.8	19.3	649	12	BG461295
8	151.4	16.5	478	12	BG145683
9	148	16.1	293	12	RG221739
10	146.2	15.9	2774	11	AK041317
11	142	15.5	834	9	AJ455645
12	111	12.1	680	14	CA355790
13	104.4	11.4	844	14	CA365628
14	83.6	9.1	661	13	BY748361
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16	72.2	7.9	733	13	CA050323
17	71.4	7.8	648	14	CB514350
18	70	7.6	659	13	BQ563030
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20	69.8	7.6	879	29	AY410745
21	69.4	7.6	866	14	CD246184
22	69.4	7.6	980	12	BM543468
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27	60	6.5	450	14	CA576592
28	60	6.5	607	10	BB634972
29	60	6.5	689	13	BY751880
30	59.8	6.5	2919	11	AK038620
31	59.8	6.5	2959	11	AK079529
32	59	6.4	695	13	BY751732
33	58	6.3	791	14	CD559646
34	58	6.3	792	14	CD559647
35	58	6.3	792	14	CD559648
36	57.6	6.3	631	14	CB476420
37	57	6.2	895	14	CB565888
38	55.8	6.1	553	10	BB636445
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41	55.2	6.0	640	10	BE198338
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43	54.2	5.9	654	10	AW373832
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#### ALIGNMENTS

RESULT 1  
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LOCUS AG145972 Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey  
DEFINITION AG145972 Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey  
ACCESSION AG145972.1 GI:16675650  
VERSION AG145972.1  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of Library RPCI-43  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 684)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpansec@cc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

Homo sapiens.  
Key Location/Qualifiers  
CDS 381..1400  
/\*tag= a  
/product= "Human GCRC-6 protein"

WO200226825-A2.

04-APR-2002.

28-SEP-2001; 2001WO-US030661.

29-SEP-2000; 2000US-0235546P.

13-OCT-2000; 2000US-0240589P.

20-OCT-2000; 2000US-024223P.

20-OCT-2000; 2000US-024232P.

03-NOV-2000; 2000US-024585P.

03-NOV-2000; 2000US-024590P.

09-NOV-2000; 2000US-024758P.

15-NOV-2000; 2000US-024934P.

(INCY-) INCYTE GENOMICS INC.

WPI; 2002-426012/45.

P-PSDB; AAE23414.

Novel G-protein coupled receptor polypeptides referred as GCRC peptides, useful for treating multiple sclerosis, cholecystitis heart failure, angina pectoris, rheumatoid arthritis, obesity, osteoporosis.

Claim 83; Page 140; 147pp; English.

The invention relates to human G-protein coupled receptor (GCRC 1-16) polypeptides and polynucleotides. Sequences of the invention are useful for the diagnosis, treatment and prevention of cell proliferative (e.g. cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris, heart failure), gastrointestinal (e.g. anorexia, cholecystitis), autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis) and metabolic disorders (e.g. obesity, osteoporosis), viral infections, atherosclerosis and hepatitis. GCRC proteins are useful for identifying compounds that modulate mimic and block olfactory and taste sensations. They are also useful for identifying GCRC modulators. GCRC DNAs are useful in gene therapy. The present sequence is human GCRC-6 cDNA

Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;

Query Match 97.5%; Score 895; DB 6; Length 1499;

Best Local Similarity 99.9%; Pred. No. 3e-254; Mismatches 0; Indels 1; Gaps 1;

Matches 906; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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381 ATGCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCACCTTA 440

61 ATCAGCCTCTACTCATAGTGCTTATGGGGGCTGGGGTGCTATTCCATTCTTTTC 120

441 ATCAGCCTCTACTCATAGTGCTTATGGGGGCTGGGGTGCTATTCCATTCTTTTC 500

121 CTCCTGGTGAATGAACCCGGTCAGTGACCAACCATGGCGGTCAATTAACCTGGTGGT 180

501 CTCCTGGTGAATGAACCCGGTCAGTGACCAACCATGGCGGTCAATTAACCTGGTGGT 560

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DB 861 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 920  
QY 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 600  
DB 921 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 980  
QY 601 GTCTTCATATATGATGATGTCAGAGCTACGCCACTCTTTTACTATCCACACAGGAG 660  
DB 981 GTCTTCATATATGATGATGTCAGAGCTACGCCACTCTTTTACTATCCACACAGGAG 1040  
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Job time : 455 secs

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 XX  
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 XX  
 PD 12-SEP-2002.  
 XX  
 PD 28-FEB-2002; 2002WO-US006455.  
 XX  
 PF 01-MAR-2001; 2001US-0272677P.  
 XX  
 PR (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PA Glucksmann MA;  
 XX  
 PI WPI: 2002-732793/79.  
 XX  
 DR P-PSDB; AAO22919.  
 DR  
 XX  
 PT New G-protein coupled receptor used in receptor assays as a target for  
 PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
 PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
 PT disorders.  
 PT  
 XX Claim 5; Page 101-103; 105pp; English.  
 PS  
 XX The invention relates to an isolated polypeptide, which is a G-protein  
 CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
 CC receptor type proteins (GPCRs), designated the 93870 receptor. The  
 CC polypeptides, nucleic acid molecules and antibodies of the invention are  
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
 CC monitoring clinical trials or pharmacogenetics), or in methods of  
 CC treatment (e.g. therapeutic and prophylactic). They are useful in  
 CC treating and diagnosing conditions related to aberrant activity or  
 CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
 CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
 CC disorders, or bone marrow mononuclear disorders, as well as cellular  
 CC proliferative and/or differentiative disorders, hormonal disorders, liver  
 CC neurological disorders, cardiovascular disorders, viral diseases, liver  
 CC disorders, and pain and metabolic disorders. Conditions that can be  
 CC treated include cancer, diabetes mellitus, hypothyroidism, bacterial or  
 CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or  
 CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,  
 CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,  
 CC Huntington's disease, heart failure, angina pectoris, myocardial  
 CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
 CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
 CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
 CC transgenic animals are useful for studying the function and/or activity  
 CC of a 93870 protein and for identifying and/or evaluating modulators of  
 CC 93870 activities. The polynucleotides of the invention can be used in  
 CC gene therapy. This polynucleotide sequence represents the 939 nucleotide  
 CC DNA of the human G-protein coupled receptor type protein of the invention  
 XX  
 SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;  
 Query Match 99.5%; Score 913.4; DB 6; Length 939;  
 Best Local Similarity 99.9%; Pred. No. 8.1e-260;  
 Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 QY 421 ACGTGTGTGATGTCATGTTGATGCTGCTGACAGATACCTCATCTTCTTCAAGATGC 480  
 Db 445 ACGTGTGTGATGTCATGTTGATGCTGCTGACAGATACCTCATCTTCTTCAAGATGC 504  
 QY 481 TACATGAGGAGCACTGCTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540  
 Db 505 TACATGAGGAGCACTGCTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 564  
 QY 541 ATCAACTATATGATGATGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 600  
 Db 565 ATCAACTATATGATGATGATGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 624  
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 Db 625 GTCTTTCATCATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 684  
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 QY 721 TACAGATTTTATAGGATCTATCTTGAATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 780  
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 Db 925 TGTGTTTGTGCGGT 939  
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 DT 27-AUG-2002 (first entry)  
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 KW cell proliferative disorder; gastrointestinal; autoimmune; metabolic;  
 KW neurological; inflammatory; cardiovascular; viral infection; anorexia;  
 KW cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;  
 KW Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;  
 KW rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;  
 KW osteoporosis; gene; ss.  
 XX

XX Glucksmann MA;  
XX WPI: 2002-732793/79.  
DR P-PSDB; AAO22919.  
XX  
PT New G-protein coupled receptor used in receptor assays as a target for  
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
PT disorders.  
XX  
PS Claim 5; Page 99-100; 105pp; English.  
XX  
CC The invention relates to an isolated polypeptide, which is a G-protein  
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled  
CC receptor type proteins (GPCRs), designated the 93870 receptor. The  
CC polypeptides, nucleic acid molecules and antibodies of the invention are  
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
CC monitoring clinical trials or pharmacogenetics), or in methods of  
CC treating (e.g. therapeutic and prophylactic). They are useful in  
CC treating and diagnosing conditions related to aberrant activity or  
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
CC disorders, or bone marrow mononuclear disorders, as well as cellular  
CC proliferative and/or differentiative disorders, hormonal disorders,  
CC neurological disorders, cardiovascular disorders, viral diseases, liver  
CC disorders, and pain and metabolic disorders. Conditions that can be  
CC treated include cancer, diabetes mellitus, hypothyroidism,  
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or  
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,  
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,  
CC Huntington's disease, heart failure, angina pectoris, myocardial  
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
CC transgenic animals are useful for studying the function and/or activity  
CC of a 93870 protein and for identifying and/or evaluating modulators of  
CC 93870 activities. The polynucleotides of the invention can be used in  
CC gene therapy. This polynucleotide sequence represents the cDNA of the  
CC 1684 nucleotide human G-protein coupled receptor type protein of the  
CC invention  
XX  
SQ Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;  
Query Match 99.8%; Score 916.4; DB 6; Length 1684;  
Best Local Similarity 99.9%; Pred No. 1.4e-260;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGCGATCCCTATAGTGACACCCACCTTA 60  
DB 171 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGCGATCCCTATAGTGACACCCACCTTA 230  
QY 61 ATCAGCCTTACTTCATAGTGCTTATTCGGCGCTGGTGGGTGCTATTTCCATTTCTTTC 120  
DB 231 ATCAGCCTTACTTCATAGTGCTTATTCGGCGCTGGTGGGTGCTATTTCCATTTCTTTC 290  
QY 121 CTCCTGGTGAATAAGAACACCCGGTCAGTGACACCCATGGCGGTCAATTAACCTGGTGTG 180  
DB 291 CTCCTGGTGAATAAGAACACCCGGTCAGTGACACCCATGGCGGTCAATTAACCTGGTGTG 350  
QY 181 GTCCACAGGTTTTCTGCTGACAGTGCCATTCCTTGACCTACTCATCAAGAGACT 240  
DB 351 GTCCACAGGTTTTCTGCTGACAGTGCCATTCCTTGACCTACTCATCAAGAGACT 410  
QY 241 TGGATGTTGGGCTGCCCTTCGAAATTTGTGAGTGCCATGCTGCACATCCACATGATAC 300  
DB 411 TGGATGTTGGGCTGCCCTTCGAAATTTGTGAGTGCCATGCTGCACATCCACATGATAC 470  
QY 301 CTCAGGTTCTTATTCATAGTGCTGATTCCTGGTCCAGATACCTCATCTTCTCAAGTGC 360  
DB 471 CTCAGGTTCTTATTCATAGTGCTGATTCCTGGTCCAGATACCTCATCTTCTCAAGTGC 530  
QY 361 AAAGACAAAGTGAATTCCTACAGAAATCTGCATGCTGTGGCTGCCAGTGGCATGTGG 420

DB 531 AAAGACAAAGTGAATTCCTACAGAAATCTGCATGCTGTGGCTGCCAGTGTGGCATGTGG 590  
QY 421 ACCTGGTGTATTCATTTGGTGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGAA 480  
DB 591 ACCTGGTGTATTCATTTGGTGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGAA 650  
QY 481 TACAATGAGGAGACATGTTTAAATTTCAAAAGAGCTTGTACACATATGGAATTC 540  
DB 651 TACAATGAGGAGACATGTTTAAATTTCAAAAGAGCTTGTACACATATGGAATTC 710  
QY 541 ATCAACTATATGATGATTCATTTTGTGCATAGCCGTTGCTGTGATTCCTGTGGTCTTCCAG 600  
DB 711 ATCAACTATATGATGATTCATTTTGTGCATAGCCGTTGCTGTGATTCCTGTGGTCTTCCAG 770  
QY 601 GTCTTCATCATTTATGTTGTTGTCAGAAAGCTACGCCACTTTTACTATCCACAGGAG 660  
DB 771 GTCTTCATCATTTATGTTGTTGTCAGAAAGCTACGCCACTTTTACTATCCACAGGAG 830  
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTGATCCTGTTGTTTCTTCCCTCC 720  
DB 831 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTGATCCTGTTGTTTCTTCCCTCC 890  
QY 721 TACCAGTTCCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 780  
DB 891 TACCAGTTCCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCTGTAGCAGC 950  
QY 781 AAGTTGCATTTTATACGAAATCTTCTCTGAGTGTACAGCAATAGCTGCTATGATTG 840  
DB 951 AAGTTGCATTTTATACGAAATCTTCTCTGAGTGTACAGCAATAGCTGCTATGATTG 1010  
QY 841 CTCTCTCTTCTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
DB 1011 CTCTCTCTTCTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1070  
QY 901 TGTGTTTGTGCGCTTAG 918  
DB 1071 TGTGTTTGTGCGCTTAG 1088  
RESULT 14  
AAL53414  
ID AAL53414 standard; DNA; 939 BP.  
XX AC AAL53414;  
XX AC AAL53414;  
XX AC AAL53414;  
DT 12-DEC-2002 (first entry)  
XX DE 939 nt coding DNA of a human G-protein coupled receptor type protein.  
XX Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;  
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;  
XX antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;  
XX cardiant; dermatological; antifertility; hepatotropic; antiallergic;  
XX antipsoriatic; ophthalmological; anisanginal; antithyroid; anticonvulsant;  
XX antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;  
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;  
XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;  
XX cellular proliferative; differentiative disorder; hormonal disorder;  
XX neurological disorder; cardiovascular disorder; viral disease; pain;  
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;  
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;  
XX viral meningitis; fungal meningoencephalitis; multiple sclerosis;  
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;  
XX Huntington's disease; heart failure; angina pectoris; dermatitis;  
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;  
XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;  
XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;  
XX transgenic animal; human; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH

XX PS Claim 1; Page 6; 58pp; English.

XX CC The invention relates to a G protein-coupled receptor (GPCR) IGS70

XX CC polypeptide including sequences that are 98-99.6% identical. Also

XX CC included are the polynucleotide encoding IGS70 (including sequences 98-

XX CC 99.6% identical to the polynucleotide or the DNA insert contained in

XX CC plasmid CBS 109818), a hybridisation probe derived from the

XX CC polynucleotide, a DNA or RNA expression system producing IGS70, a host

XX CC comprising the expression system, IGS70 receptor membrane preparation

XX CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is

XX CC useful for diagnosing a disease or a susceptibility to disease in a

XX CC subject related to expression or activity of the IGS70 polypeptide in a

XX CC subject by determining the presence or absence of mutation in the

XX CC nucleotide sequence encoding IGS70 in the genome of the subject in a

XX CC sample derived from the subject. IGS70 is also useful identifying agonist

XX CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified

XX CC ant/agonists are useful for treating psychiatric and central nervous

XX CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,

XX CC multiple sclerosis, anxiety, cardiovascular diseases such as heart

XX CC failure, angina pectoris, myocardial infarction, kidney disease such as

XX CC renal failure, gastrointestinal disorders such as irritable bowel

XX CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,

XX CC inflammation, cancers, asthma, infection (such as bacterial, viral,

XX CC fungal, protozoal) especially human immunodeficiency virus infection

XX CC (HIV), diabetes, osteoporosis and allergies. The present sequence encodes

XX CC the human GPCR IGS70

SQ Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 99.8%; Score 916.4; DB 6; Length 1051;

Best Local Similarity 99.9%; Pred. No. 1.1e-260;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATCCCTCCAGAAATCTCTTGGCATCTCTATAGTGACACCCCACTTA 60

DB 60 ATGCTGGCCACAAATCCCTCCAGAAATCTCTTGGCATCTCTATAGTGACACCCCACTTA 119

QY 61 ATCAGCTCTACTTCTAGTGTCTTATGGCGGCTGGTGGTCTCATTTCCATCTTTTC 120

DB 120 ATCAGCTCTACTTCTAGTGTCTTATGGCGGCTGGTGGTCTCATTTCCATCTTTTC 179

QY 121 CTCTCTGGTGAATGAACACCCCGTCAAGTACACCAATGGCGTCTTAATCTTGGTGGTG 180

DB 180 CTCTCTGGTGAATGAACACCCCGTCAAGTACACCAATGGCGTCTTAATCTTGGTGGTG 239

QY 181 GTCCACAGGTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 240

DB 240 GTCCACAGGTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 299

QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGCACATCCACATGTAC 300

DB 300 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGCACATCCACATGTAC 359

QY 301 CTCACGTTCTTCTATGTGGTGATCTGTGTCACCAAGATACCTCATCTTCTCAAGTGC 360

DB 360 CTCACGTTCTTCTATGTGGTGATCTGTGTCACCAAGATACCTCATCTTCTCAAGTGC 419

QY 361 AAAGACAAAGTGGAAATCTTACAGAAATCTGCTGTGGTCCAGTGTCTGGCATGTGG 420

DB 420 AAAGACAAAGTGGAAATCTTACAGAAATCTGCTGTGGTCCAGTGTCTGGCATGTGG 479

QY 421 ACCTGGTGAATGTGATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480

DB 480 ACCTGGTGAATGTGATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 539

QY 481 TACAATGAGGAGCAGTGTGTTAAATTTCAAGAGCTTGTCTTACACATATGTGAATTC 540

DB 540 TACAATGAGGAGCAGTGTGTTAAATTTCAAGAGCTTGTCTTACACATATGTGAATTC 599

QY 541 ATCAACTATATGATGATCAATTTTGTCTATGACCGTGTCTGTGATCTGTGTTCCAG 600

DB 600 ATCAACTATATGATGATCAATTTTGTCTATGACCGTGTCTGTGATCTGTGTTCCAG 659

QY 601 GTCTTCATCATTTATGTTGATGGTGCAGAGCTAGCCACCTCTTTTACTATCCACAGGAG 660

DB 660 GTCTTCATCATTTATGTTGATGGTGCAGAGCTAGCCACCTCTTTTACTATCCACAGGAG 719

QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720

DB 720 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 779

QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTCTGACGCAATTCGAATGCTGTAAACAGC 780

DB 780 TACCAGTTCTTTAGGATCTATTACTTGAATGTTCTGACGCAATTCGAATGCTGTAAACAGC 839

QY 781 AAGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTG 840

DB 840 AAGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTG 899

QY 841 CTCTCTCTTTGCTTTGGGGGAAGCCATGTTTAAAGCAAAAGATAAATGGCTTATGAAT 900

DB 900 CTCTCTCTTTGCTTTGGGGGAAGCCATGTTTAAAGCAAAAGATAAATGGCTTATGAAT 959

QY 901 TGTGTTTGTCCCGTTAG 918

DB 960 TGTGTTTGTCCCGTTAG 977

RESULT 13

AAL53413

ID AAL53413 standard; cDNA; 1684 BP.

AC AAL53413;

DT 12-DEC-2002 (first entry)

DE 1684 nt cDNA of human G-protein coupled receptor type protein.

KW Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory;

KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;

KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;

KW cardiant; dermatological; antiinfertility; hepatotropic; antiallergic;

KW antipsoriatic; ophthalmologic; antiangular; antithyroid; anticonvulsant;

KW anirhematic; antiarthritic; G-protein coupled receptor; subfamily 1;

KW 93870 receptor; immune; inflammatory disorder; bone marrow mononuclear disorder;

KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;

KW cellular proliferation; differentiative disorder; hormonal disorder;

KW neurological disorder; cardiovascular disorder; viral disease; pain;

KW liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;

KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;

KW viral meningitis; fungal meningoencephalitis; multiple sclerosis;

KW Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;

KW Huntington's disease; heart failure; angina pectoris; dermatitis;

KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;

KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;

KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;

KW transgenic animal; human; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers

CDS 147..1088

/tag= a

/product= "Human G-protein coupled receptor type protein

93870"

PN WO200270657-A2.

XX 12-SEP-2002.

PD 28-FEB-2002; 2002WO-US006455.

XX 01-MAR-2001; 2001US-0272677P.

PR (MILL-) MILLENNIUM PHARM INC.

PA

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XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX WPI; 2003-315783/31.
XX
XX P-PSDB; ADC86555.
XX
XX
XX New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1007; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The
XX polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
XX invention.
XX
XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 918; DB 9; Length 113306;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-260;
XX Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGCGTGGCCCAATACCTCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
XX 11540 ATGCGTGGCCCAATACCTCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 11599
XX
XX 61 ATCAGCCTCTACTTCATAGTGTCTTATGCGGGTGGTGGTGCATTCATTCCTTTTC 120
XX 11600 ATCAGCCTCTACTTCATAGTGTCTTATGCGGGTGGTGGTGCATTCATTCCTTTTC 11659
XX
XX 121 CTCCTGTGTAATAAGAACACCCGGTCACTGACACCACTGGCGGTCAATTAATTCGGTGTG 180
XX 11660 CTCCTGTGTAATAAGAACACCCGGTCACTGACACCACTGGCGGTCAATTAATTCGGTGTG 11719
XX
XX 181 GTCCACAGCGTTTTCTGCTGACAGTGCCATTCGCTTGACCTACCTCATCAAGAAGACT 240
XX 11720 GTCCACAGCGTTTTCTGCTGACAGTGCCATTCGCTTGACCTACCTCATCAAGAAGACT 11779
XX
XX 241 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
XX 11780 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 11839
XX
XX 301 CTCAGTTCCTATTCATGTGGTGAATCTGTGCTACCAAGATACCTCATCTTCTCAAGTGC 360
XX 11840 CTCAGTTCCTATTCATGTGGTGAATCTGTGCTACCAAGATACCTCATCTTCTCAAGTGC 11899
XX
XX 361 AAGACAAAGTGGAAATCTCAGAAATCTGATGCTGGCTGCAGTGGCTGGCATGTGG 420
XX 11900 AAGACAAAGTGGAAATCTCAGAAATCTGATGCTGGCTGCAGTGGCTGGCATGTGG 11959
XX
XX 421 ACGTGTGTATGTTCATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
XX 11960 ACGTGTGTATGTTCATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 12019
XX
XX 481 TACATGAGGAGCACTGTTTAAATTTACAAAGCTTGGCTTACATATGTGAAATC 540
XX 12020 TACATGAGGAGCACTGTTTAAATTTACAAAGCTTGGCTTACATATGTGAAATC 12079
XX
XX 541 ATCAACTATATATAGTATCATTTTGTGTCATAGCCGTTGCTGTGATTCGTGGTCTTCCAG 600
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Db 12080 ATCAACTATATAGTATCATTTTGTGTCATAGCCGTTGCTGTGATTCGTGGTCTTCCAG 12139
Qy 601 GTCTTCATCATTTATGTTGATGGTGCAAGAGCTACGCCACTCTTTTACTATCCCAACAGGAG 660
Db 12140 GTCTTCATCATTTATGTTGATGGTGCAAGAGCTACGCCACTCTTTTACTATCCCAACAGGAG 12199
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720
Db 12200 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCCTCC 12259
Qy 721 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCCGTGTACAGC 780
Db 12260 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCCGTGTACAGC 12319
Qy 781 AAGGTTGCATTTTATAACGAAATCTTCTTACGAGTGAACGCAATTAAGCTGCTATGATTG 840
Db 12320 AAGGTTGCATTTTATAACGAAATCTTCTTACGAGTGAACGCAATTAAGCTGCTATGATTG 12379
Qy 841 CTCTCTCTTCTCTTGGGGGAAGCCATTCGTTTAAACCAAGATAATTCGCTTATGGAAT 900
Db 12380 CTCTCTCTTCTCTTGGGGGAAGCCATTCGTTTAAACCAAGATAATTCGCTTATGGAAT 12439
Qy 901 TGTGTTTGTGCGCGTTAG 918
Db 12440 TGTGTTTGTGCGCGTTAG 12457

RESULT 12
ABK87351
ID ABK87351 standard; cDNA; 1051 BP.
XX
AC ABK87351;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human cDNA encoding G protein-coupled receptor IGS70.
XX
KW Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS;
KW psychiatric disorder; central nervous system disorder; schizophrenia;
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
KW heart failure; angina pectoris; myocardial infarction; kidney disease;
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
KW osteoporosis; allergy.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 60..977
FT /*tag= a
FT /product= "GPCR IGS70"
XX
PN WO200244212-A2.
XX
XX 06-JUN-2002.
XX
XX 23-NOV-2001; 2001WO-EP013706.
XX
XX 30-NOV-2000; 2000EP-00204280.
XX 05-DEC-2000; 2000US-0251045P.
XX
XX (SOLV ) SOLVAY PHARM BV.
XX
XX Deleersnijder W, Blockx H, De Moor L;
XX
XX WPI; 2002-527703/56.
XX P-PSDB; AAU99179.
XX
XX Novel G-protein coupled receptor IGS70 polypeptide useful for treating
XX dysfunctions, disorders or disease related to lung, bone marrow, spinal
XX cord immune system.
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XX Human; gene; ds; G protein-coupled receptor; GPCR; nPCR; beGPCR;  
 KW nG protein coupled receptor; communication; serpentine structure;  
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;  
 KW genetic predisposition; brain; immune response; gene therapy;  
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;  
 KW Huntington's disease; Alzheimer's disease; manic depression; stroke;  
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;  
 KW tranquilizer.  
 XX Homo sapiens.  
 XX W0200264789-A1.  
 XX 22-AUG-2002.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX (PHAA ) PHARMACIA & URJOHN CO.  
 XX Lind P, Parodi LA, Vogeli G, Wood LS;  
 XX WPI; 2002-674879/72.  
 XX P-PSDB; ABG93787.  
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,  
 PT useful for treating or diagnosing a mental disorder or a disorder  
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or  
 PT Parkinson's disease.  
 XX Example 1; Page 84-85; 244pp; English.  
 XX The invention discloses an isolated human polypeptide, and encoding  
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the  
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the  
 CC communication between cells and their environment and are characterised  
 CC by a serpentine structure that passes through the cell membrane seven  
 CC times, hence the reason such receptors are sometimes called seven  
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are  
 CC useful for identifying an nGPCR allelic variant that correlates with a  
 CC mental disorder, for isolating an antibody that binds to an epitope of  
 CC the polypeptide, and for identifying a compound that binds the polypeptide or  
 CC polynucleotide and/or modulates its biological activity, for screening a  
 CC human subject to diagnose a disorder, or a genetic predisposition to a  
 CC disorder, affecting the brain or a genetic disposition to the disorder,  
 CC for identifying compounds useful for the treatment of a mental disorder,  
 CC and for identifying a compound useful as a modulator of binding between  
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also  
 CC useful for inducing an immune response in a mammal. The nucleic acid or  
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.  
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,  
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's  
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also  
 CC be used for treating diabetes, inflammation or wounds. The sequences  
 CC presented in ABS70202-ABS70248, ABS70238 and ABS70243 are the DNAs  
 CC encoding the nGPCRs (also referred to as beGPCRs)  
 XX SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 918; DB 6; Length 2525;  
 Best Local Similarity 100.0%; Pred. No. 6e-261;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGCTGGCCACAACTACTCCAGAAATCTCTTGGGATCCTATAGTACACCCCACTTA 60  
 27 ATGCTGGCCACAACTACTCCAGAAATCTCTTGGGATCCTATAGTACACCCCACTTA 86  
 61 ATGAGCTCTACTTTCATAGTGCCTATTGGGGGCTGGTGGTGCATTTCCATTCTTTC 120  
 87 ATGAGCTCTACTTTCATAGTGCCTATTGGGGGCTGGTGGTGCATTTCCATTCTTTC 146

QY 121 CTCCTGGTGAATAAGAACACCCGGTCACTGAGTACCACCATGCGGTCAATTAATCTGGTGGT 180  
 DB 147 CTCCTGGTGAATAAGAACACCCGGTCACTGAGTACCACCATGCGGTCAATTAATCTGGTGGT 206  
 QY 181 GTCACACAGGTTTTCTCTGCTGACAGTGCATTTGCTTGACTACCTCATCAAGAAGACT 240  
 DB 207 GTCCACAGGTTTTCTCTGCTGACAGTGCATTTGCTTGACTACCTCATCAAGAAGACT 266  
 QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCAATCCACATGATGAC 300  
 DB 267 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCAATCCACATGATGAC 326  
 QY 301 CTCAGGTTCCCTATTCTATGCTGGTGCATCTGCTGACAGTACCTCATCTTCTCAAGTGC 360  
 DB 327 CTCAGGTTCCCTATTCTATGCTGGTGCATCTGCTGACAGTACCTCATCTTCTCAAGTGC 386  
 QY 361 AAAGACAAAGTGGAAATCTCAGAAAACTGCATGCTGTGGCTGCGAGTGGCATGATGG 420  
 DB 387 AAAGACAAAGTGGAAATCTCAGAAAACTGCATGCTGTGGCTGCGAGTGGCATGATGG 446  
 QY 421 AGCTGGTGAATGTCATTTGCTGCTACCCCTGCTCTCCCGTATGGAATCCATGAGAA 480  
 DB 447 AGCTGGTGAATGTCATTTGCTGCTACCCCTGCTCTCCCGTATGGAATCCATGAGAA 506  
 QY 481 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTTACACATATGTGAAAAATC 540  
 DB 507 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTTACACATATGTGAAAAATC 566  
 QY 541 ATCAACTATATGATAGTCAATTTTGTGCTAGCCGTTGCTGATTCGTGGTCTTCAG 600  
 DB 567 ATCAACTATATGATAGTCAATTTTGTGCTAGCCGTTGCTGATTCGTGGTCTTCAG 626  
 QY 601 GTCCTTCATCATTTATGCTGATGCTGAGAAAGTACGCCACTCTTTACTATCCACAGAG 660  
 DB 627 GTCCTTCATCATTTATGCTGATGCTGAGAAAGTACGCCACTCTTTACTATCCACAGAG 686  
 QY 661 TTCTGGGCTCAGTGAATAAACCCTATTTTATAGGGTCACTCTGTTGTTGTTCTTCCC 720  
 DB 687 TTCTGGGCTCAGTGAATAAACCCTATTTTATAGGGTCACTCTGTTGTTGTTCTTCCC 746  
 QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAAACAGC 780  
 DB 747 TACCAGTTCTTTAGGATCTATTCTTGAATGTTGTGACGCAATTCGAATGCTGTAAACAGC 806  
 QY 781 AAGTTGCAATTTATACGAAATCTTTTGTAGTGTAAACAGCAATAGCTGCTATGATTG 840  
 DB 807 AAGTTGCAATTTATACGAAATCTTTTGTAGTGTAAACAGCAATAGCTGCTATGATTG 866  
 QY 841 CTTCTCTTTGCTTTGGGGGAGCCATGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
 DB 867 CTTCTCTTTGCTTTGGGGGAGCCATGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926  
 QY 901 TGTGTTTTGTCGCGTTAG 918  
 DB 927 TGTGTTTTGTCGCGTTAG 944  
 RESULT 11  
 ADC86554  
 ID ADC86554 standard; DNA; 113306 BP.  
 XX AC ADC86554;  
 XX AC ADC86554;  
 DT 01-JAN-2004 (first entry)  
 XX DE Human GPCR gene SEQ ID NO:1007.  
 XX ds; gene; human; GPCR;  
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.  
 XX Homo sapiens.  
 XX EP1270724-A2.  
 PN

neurological disorder; neuronal disorder; Alzheimer's disease; cancer;  
attention deficit-hyperactivity disorder/attention deficit disorder;  
Parkinson's disease; migraine; senile dementia; inflammatory disease;  
rheumatoid arthritis; autoimmune disorder; respiratory ailment;  
neuroprotective; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200136473-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000WO-US031581.  
XX  
PR 16-NOV-1999; 99US-0165838P.  
PR 17-NOV-1999; 99US-0166071P.  
PR 19-NOV-1999; 99US-0166678P.  
PR 28-DEC-1999; 99US-0173396P.  
PR 22-FEB-2000; 2000US-0184129P.  
PR 28-FEB-2000; 2000US-0185421P.  
PR 28-FEB-2000; 2000US-0185554P.  
PR 02-MAR-2000; 2000US-0186530P.  
PR 03-MAR-2000; 2000US-0186811P.  
PR 09-MAR-2000; 2000US-0188114P.  
PR 17-MAR-2000; 2000US-0190310P.  
PR 21-MAR-2000; 2000US-0190800P.  
PR 20-APR-2000; 2000US-0198568P.  
PR 02-MAY-2000; 2000US-0201190P.  
PR 08-MAY-2000; 2000US-0203111P.  
PR 25-MAY-2000; 2000US-0207094P.  
XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;  
PI Schellin KA, Kaytes PS, Bannigan CW, Ruff V, Sejlitz T, Ruff RM;  
XX  
DR WPI; 2001-389826/41.  
DR P-PSDB; AAG80969.  
XX  
PT New G protein-coupled receptor (nGPR-x) and its encoding polynucleotide  
PT useful for diagnosing and treating e.g. schizophrenia.  
XX  
PS Claim 4; Page 89-90; 261pp; English.  
XX  
CC The present invention relates to novel G protein-coupled receptors  
CC (nGPRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,  
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is  
CC the coding sequence for one such G protein-coupled receptor. GPCRs are  
CC also known as seven transmembrane receptors and function in signal  
CC transduction. The nGPRx coding sequences are useful for screening a  
CC human to diagnose a disorder affecting the brain or a genetic  
CC predisposition, specifically schizophrenia. nGPRx are useful for  
CC identifying compounds useful for treating schizophrenia. Detection of  
CC nGPRx in a sample is useful as a diagnostic tool for diseases or  
CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,  
CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular  
CC diseases, proliferative disorders and hormonal disorders. Modulators of  
CC nGPRx activity have the utility for treating neurological disorders,  
CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity  
CC disorder/attention deficit disorder), and neuronal disorders such as  
CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.  
CC Additional disorders include inflammatory conditions (e.g. Crohn's  
CC disease), rheumatoid arthritis, autoimmune disorders, cancers,  
CC respiratory ailments such as asthma, and inflammatory diseases e.g.  
CC inflammatory bowel disease  
XX  
SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;  
Query Match 100.0%; Score 918; DB 4; Length 2525;  
Best Local Similarity 100.0%; Pred. No. 6e-261;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCCTGGCCCAATACCTCCAGGAATTCCTTTCGATCCTATAGTGACACCCCACTTA 60

Db 27 ATGCCTGGCCCAATACCTCCAGGAATTCCTTTCGATCCTATAGTGACACCCCACTTA 86  
Qy 61 ATCAGCCTCTACTTCTATAGTGCTTATTTGGGGGCTGTGGTGTCAATTTCCATTCCTTTTC 120  
Db 87 ATCAGCCTCTACTTCTATAGTGCTTATTTGGGGGCTGTGGTGTCAATTTCCATTCCTTTTC 146  
Qy 121 CTCCTGGTGAATGAACACCCGGTCAGTGAACACCATGCGGTCAATTAACCTTGGTGGT 180  
Db 147 CTCCTGGTGAATGAACACCCGGTCAGTGAACACCATGCGGTCAATTAACCTTGGTGGT 206  
Qy 181 GTCCACAGCGCTTTCTGCTGACAGTGCCTATTTGCGTGTGACCTACCTCATCAAGAGACT 240  
Db 207 GTCCACAGCGCTTTCTGCTGACAGTGCCTATTTGCGTGTGACCTACCTCATCAAGAGACT 266  
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300  
Db 267 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 326  
Qy 301 CTCACGTTCTATTCATGTTGATCTGCTGTCACAGATACCTCATCTCTTCAAGTGC 360  
Db 327 CTCACGTTCTATTCATGTTGATCTGCTGTCACAGATACCTCATCTCTTCAAGTGC 386  
Qy 361 AAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 420  
Db 387 AAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 446  
Qy 421 ACGCTGGTGAATTCATGTTGTTGTTACCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 480  
Db 447 ACGCTGGTGAATTCATGTTGTTGTTACCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 506  
Qy 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGGAATTC 540  
Db 507 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGGAATTC 566  
Qy 541 ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG 600  
Db 567 ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG 626  
Qy 601 GTCTTCATCATATGTTGATGTTGTCAGAGACTACGCCACTCTTACTATCCACACAGGAG 660  
Db 627 GTCTTCATCATATGTTGATGTTGTCAGAGACTACGCCACTCTTACTATCCACACAGGAG 686  
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTTCATCTTGTGTTGTTCTTCCC 720  
Db 687 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTTCATCTTGTGTTGTTCTTCCC 746  
Qy 721 TACAGTCTTTTAGGATCTATTAATTTGAATGTTGTGACGATCCAAATGCGCTGTAACGC 780  
Db 747 TACCAGTCTTTTAGGATCTATTAATTTGAATGTTGTGACGATTCCAATGCGCTGTAACGC 806  
Qy 781 AAGTTGCAATTTTATAACGAAATCTTCTGAGTGTAAACAGCAATTAAGCTGCTATGATTG 840  
Db 807 AAGTTGCAATTTTATAACGAAATCTTCTGAGTGTAAACAGCAATTAAGCTGCTATGATTG 866  
Qy 841 CTTCCTCTTCTTTCGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
Db 867 CTTCCTCTTCTTTCGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926  
Qy 901 TGTGTTTGTGCGGTTAG 918  
Db 927 TGTGTTTGTGCGGTTAG 944  
RESULT 10  
ABS70242  
ID ABS70242 standard; DNA: 2525 BP.  
XX AC ABS70242;  
XX XX  
DT 26-NOV-2002 (first entry)  
XX XX  
DE DNA encoding human G protein-coupled receptor, nGPR-16.

XX 19-NOV-2002 (first entry)  
 XX Human GREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.  
 DE  
 XX GREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
 KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
 KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
 KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
 KW Parkinson's disease; Crohn's disease; constipation; infection;  
 KW gene therapy; gene; ss.  
 XX Homo sapiens.  
 XX WO200263004-A2.  
 XX 15-AUG-2002.  
 XX 06-FEB-2002; 2002WO-US003635.  
 XX 07-FEB-2001; 2001US-0267322P.  
 XX 23-FEB-2001; 2001US-0271215P.  
 XX 08-MAR-2001; 2001US-0274551P.  
 XX 23-MAR-2001; 2001US-0278507P.  
 XX 30-MAR-2001; 2001US-0280597P.  
 XX 02-APR-2001; 2001US-0281107P.  
 XX 06-APR-2001; 2001US-0282121P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
 PI Kallack DA, Gandhi AP, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;  
 PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Burford N, Lu DAM;  
 PI Graul RC, Khan JA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
 PI Warren BA, Yang J, Lee EA, Harland L;  
 XX WPI; 2002-627557/67.  
 DR P-PSDB; AAB71327.  
 XX New human G-protein coupled receptors (GREC), useful for diagnosing or  
 PT treating a disease or condition associated with decreased expression or  
 PT over expression of functional GRECs e.g. cancer, Alzheimer's and  
 PT Parkinson's.  
 XX Claim 115; Page 213-214; 239pp; English.  
 XX This invention describes novel polypeptides which have anti-HIV,  
 CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,  
 CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
 CC antibacterial, fungicide and protozoacide activity. The products of the  
 CC invention are useful for treating a disease or condition associated with  
 CC decreased expression or over expression of functional G-protein coupled  
 CC receptors (GREC), while antibodies generated against the polypeptide of  
 CC the invention are useful for diagnosing a condition or disease associated  
 CC with the expression of GREC e.g. arteriosclerosis, cirrhosis, cancer,  
 CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
 CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
 CC The compounds described in the invention can be used for gene therapy.  
 CC AAF8580-AAF88627 encode the GREC proteins represented by AAB71322-  
 CC AAB71369, described in the disclosure of the invention  
 XX  
 XX Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;  
 XX  
 XX Query Match 100.0%; Score 918; DB 6; Length 1460;  
 XX Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
 XX Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCCCTGGCCACAAATACCTCCAGGAATTCCTTGGGATCCTATAGTGACACCCCACTTA 60  
 DB 343 ATCCCTGGCCACAAATACCTCCAGGAATTCCTTGGGATCCTATAGTGACACCCCACTTA 402  
 QY 61 ATCAGCCTCTACTTATAGTGTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC 120

DB 403 ATCAGCCTCTACTTATAGTGTCTTATTGGCGGCTGGTGGTGTCTATTTCCATTTCTTTTC 462  
 QY 121 CTCCTGGTGAATAATGAACACCGGTAGTGACACCATGCGGTCAATTAACCTTTGGTGGTG 180  
 DB 463 CTCCTGGTGAATAATGAACACCGGTAGTGACACCATGCGGTCAATTAACCTTTGGTGGTG 522  
 QY 181 GTCCACAGCGTTTCTTCTGTGACAGTCCCAATTTGCTGTGACCTACCTCATCAGAGACT 240  
 DB 523 GTCCACAGCGTTTCTTCTGTGACAGTCCCAATTTGCTGTGACCTACCTCATCAGAGACT 582  
 QY 241 TGGATGTTGGGCTGCCCTCTGCAAAATTTGTGAGTCCCATGTGTGACATCCACATGTAC 300  
 DB 593 TGGATGTTGGGCTGCCCTCTGCAAAATTTGTGAGTCCCATGTGTGACATCCACATGTAC 642  
 QY 301 CTCACGTTCTTATTTCTATGTGGTATCCTGGTACACAGATACCTCATCTTCTTCAAGTGC 360  
 DB 643 CTCACGTTCTTATTTCTATGTGGTATCCTGGTACACAGATACCTCATCTTCTTCAAGTGC 702  
 QY 361 AAAGACAAAGTGAATTTCTACAGAAAATGCTGCTGCTGGCTGCCAGTGTGGCATGTGG 420  
 DB 703 AAAGACAAAGTGAATTTCTACAGAAAATGCTGCTGCTGGCTGCCAGTGTGGCATGTGG 762  
 QY 421 ACGTGTGTATTTGTGATGTGGTATCCCTGGTGTCTCCCGGTATGAAATCCCATGAGAA 480  
 DB 763 ACGTGTGTATTTGTGATGTGGTATCCCTGGTGTCTCCCGGTATGAAATCCCATGAGAA 822  
 QY 481 TACATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATC 540  
 DB 823 TACATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATC 882  
 QY 541 ATCACTATATGATGATGATCATTTTGTGATAGCCCTGCTGTGATCTGTGGTCTTCCAG 600  
 DB 883 ATCACTATATGATGATGATCATTTTGTGATAGCCCTGCTGTGATCTGTGGTCTTCCAG 942  
 QY 601 GTCTTCATCATTTGATGTGGTGCAGAGCTAGCCACTTTTACTATCCACCCAGAG 660  
 DB 943 GTCTTCATCATTTGATGTGGTGCAGAGCTAGCCACTTTTACTATCCACCCAGAG 1002  
 QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTTGTGTTTCTTCTTCCC 720  
 DB 1003 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTTGTGTTTCTTCTTCCC 1062  
 QY 721 TACAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGATCCCAATGCTGTGAACAGC 780  
 DB 1063 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGATCCCAATGCTGTGAACAGC 1122  
 QY 781 AAGGTTGCAATTTTATACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTG 840  
 DB 1123 AAGGTTGCAATTTTATACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTG 1182  
 QY 841 CTTCCTTTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
 DB 1183 CTTCCTTTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1242  
 QY 901 TGTGTTTGTGCGGTAG 918  
 DB 1243 TGTGTTTGTGCGGTAG 1260  
 XX  
 XX RESULT 9  
 XX AAH51009  
 XX ID AAH51009 standard; DNA; 2525 BP.  
 XX AC AAH51009;  
 XX DT 28-AUG-2001 (first entry)  
 XX DE Human nPCR16 coding sequence #2.  
 XX KW G protein-coupled receptor; nPCR; seven transmembrane receptor;  
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;  
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
 KW cardiovascular disease; proliferative disorder; hormonal disorder;

Db 1119 TGTGTTTGTGCGGTAG 1136  
 |||||  
 RESULT 7  
 AAF89584  
 ID AAF89584 standard; cDNA; 1340 BP.  
 XX  
 AC AAF89584;  
 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.  
 XX  
 KW GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
 KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
 KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
 KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
 KW Parkinson's disease; Crohn's disease; constipation; infection;  
 KW gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200263004-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US003635.  
 XX  
 PR 07-FEB-2001; 2001US-0267322P.  
 XX  
 PR 23-FEB-2001; 2001US-0271215P.  
 PR 08-MAR-2001; 2001US-0274551P.  
 PR 23-MAR-2001; 2001US-0278507P.  
 PR 30-MAR-2001; 2001US-0280597P.  
 PR 02-APR-2001; 2001US-0281107P.  
 PR 06-APR-2001; 2001US-0282121P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC..  
 XX  
 PI Baughn MR, Triboley CM, Nguyen DB, Thornton M, Yao MG;  
 PI Kallick DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;  
 PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;  
 PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
 PI Warren BA, Yang J, Lee EA, Harland L;  
 XX  
 DR WPI; 2002-627557/67.  
 XX  
 DR P-PSDB; AAB71326.  
 XX  
 PT New human G-protein coupled receptors (GCREC), useful for diagnosing or  
 PT treating a disease or condition associated with decreased expression or  
 PT over expression of functional GCRECs e.g. cancer, Alzheimer's and  
 PT Parkinson's.  
 XX  
 PS Claim 114; Page 213; 239pp; English.  
 XX  
 CC This invention describes novel polypeptides which have anti-HIV.  
 CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,  
 CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
 CC antibacterial, fungicide and protozoacide activity. The products of the  
 CC invention are useful for treating a disease or condition associated with  
 CC decreased expression or over expression of functional G-protein coupled  
 CC receptors (GCREC), while antibodies generated against the polypeptide of  
 CC the invention are useful for diagnosing a condition or disease associated  
 CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
 CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
 CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
 CC The compounds described in the invention can be used for gene therapy.  
 CC AAF89580-AAF89627 encode the GCREC proteins represented by AAB71322-  
 CC AAB71369, described in the disclosure of the invention  
 XX  
 SQ Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 918; DB 6; Length 1340;

Best Local Similarity 100.0%; Pred. No. 4.3e-261;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGCCTGGCCACAATATCTCCAGGAATTCCTCTTGGATCCTATAGTGCACCCCACTTA 60  
 Db 223 ATGCCTGGCCACAATATCTCCAGGAATTCCTCTTGGATCCTATAGTGCACCCCACTTA 282  
 Qy 61 ATCAGGCTCTACTTCATAGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 120  
 Db 283 ATCAGGCTCTACTTCATAGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 342  
 Qy 121 CTCCTGGTGAATAAGAACACCCCGTCACTGACACCAATCGCGGTCAATTAACCTGGTGGTG 180  
 Db 343 CTCCTGGTGAATAAGAACACCCCGTCACTGACACCAATCGCGGTCAATTAACCTGGTGGTG 402  
 Qy 181 GTCACAGCGTTTCTGTGACAGTGCCTATTTGGTGTGACCTCACTCATCAGAGAGACT 240  
 Db 403 GTCACAGCGTTTCTGTGACAGTGCCTATTTGGTGTGACCTCACTCATCAGAGAGACT 462  
 Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300  
 Db 463 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 522  
 Qy 301 CTCACGTTCTCTATTTATGTTGGTGTCTGTCACAGATACCTCATCTTCTTCAAGTGC 360  
 Db 523 CTCACGTTCTCTATTTATGTTGGTGTCTGTCACAGATACCTCATCTTCTTCAAGTGC 582  
 Qy 361 AAAGACAAAGTGGAAATTTCTACAGAAATTCATGCTGTGCTGCCAGTGTGCGCATGTGG 420  
 Db 583 AAAGACAAAGTGGAAATTTCTACAGAAATTCATGCTGTGCTGCCAGTGTGCGCATGTGG 642  
 Qy 421 ACGCTGGTATTTGTCATTTGTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480  
 Db 643 ACGCTGGTATTTGTCATTTGTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 702  
 Qy 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540  
 Db 703 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 762  
 Qy 541 ATCAACTATATGATAGTCACTTTTGTGCATAGCCGTTGTGTGTGATTCCTGTTGGTCTTCCAG 600  
 Db 763 ATCAACTATATGATAGTCACTTTTGTGCATAGCCGTTGTGTGTGATTCCTGTTGGTCTTCCAG 822  
 Qy 601 GTCTTCATCATTTATGTTGATGTTGTCAGAGTACGCCACTTTTACTATCCACACAGGAG 660  
 Db 823 GTCTTCATCATTTATGTTGATGTTGTCAGAGTACGCCACTTTTACTATCCACACAGGAG 882  
 Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTGTTGTTTCTTCCCTCC 720  
 Db 883 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTGTTGTTTCTTCCCTCC 942  
 Qy 721 TACAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 780  
 Db 943 TACAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 1002  
 Qy 781 AAGTTTCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTGCTATGATTG 840  
 Db 1003 AAGTTTCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTGCTATGATTG 1062  
 Qy 841 CTCTCTCTTCTCTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900  
 Db 1063 CTCTCTCTTCTCTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1122  
 Qy 901 TGTGTTTGTGCGGTAG 918  
 Db 1123 TGTGTTTGTGCGGTAG 1140  
 RESULT 8  
 AAF89585  
 ID AAF89585 standard; cDNA; 1460 BP.  
 XX  
 AC AAF89585;



QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTGTGTTTCTTCTCC 720  
 |||||  
 Db 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTGTGTTTCTTCTCC 720  
 |||||  
 QY 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGACGCATTCCTCAATGCTGTAACAGC 780  
 |||||  
 Db 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGACGCATTCCTCAATGCTGTAACAGC 780  
 |||||  
 QY 781 AAGGTTGCAATTTATAACGAAATCTTTCTGAGTGTAAACAGCAATTAAGTCTATCATTTG 840  
 |||||  
 Db 781 AAGGTTGCAATTTATAACGAAATCTTTCTGAGTGTAAACAGCAATTAAGTCTATCATTTG 840  
 |||||  
 QY 841 CTTCTCTTTGCTTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900  
 |||||  
 Db 841 CTTCTCTTTGCTTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900  
 |||||  
 QY 901 TGTGTTTGTGCGGTAG 918  
 |||||  
 Db 901 TGTGTTTGTGCGGTAG 918  
 |||||

## RESULT 5

AAL57070

ID AAL57070 standard; DNA; 1040 BP.

XX AAL57070;

XX 17-SEP-2003 (first entry)

XX Human G-protein coupled receptor GAVE18 DNA sequence.

XX Human G-protein coupled receptor; GAVE18; signal transduction;

KW inflammation; physiological immunological response; antiinflammatory;

KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;

KW chromosomal mapping; tissue typing; forensic biology;

KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;

KW rheumatoid arthritis; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..918  
 CDS /\*tag= a  
 FT /product= "GAVE18 protein"

XX WO2003042399-A2.

XX 22-MAY-2003.

XX 08-NOV-2002; 2002WO-US035887.

XX 13-NOV-2001; 2001US-0354150P.

XX 22-MAR-2002; 2002GB-00006891.

XX (AVET ) AVENTIS PHARM INC.

XX Eishengdrelo H, Cai J, Busch SJ, Gassenhuber J;

XX WPI: 2003-457496/43.

XX P-PSDB; AAO27265.

XX New GAVE18 polypeptide and nucleic acid molecule encoding the  
 PT polypeptide, useful for preventing and treating a disease or disorder  
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or  
 PT rheumatoid arthritis.  
 XX Claim 1; Fig 5; 88pp; English.  
 PS This invention relates to a novel G-protein coupled receptor (GAVE18)  
 CC that is involved in signal transduction in respect to inflammation and  
 CC the physiological immunological response. Molecules which may modulate  
 CC the signalling activity or signal transduction of the receptor may be

CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The  
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for  
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18  
 CC proteins and antibodies may be useful in screening assays, detection  
 CC assays (for example chromosomal mapping, tissue typing or forensic  
 CC biology), or predictive medicine (for example diagnostic assays,  
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The  
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse  
 CC agonist and antagonist are also useful for preventing and treating a  
 CC disease or disorder associated with aberrant expression or activity of  
 CC GAVE18, such as inflammation and immunological-related diseases or  
 CC disorders, for example asthma, chronic obstructive pulmonary disease or  
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding  
 CC the GAVE18 protein of the invention  
 XX

SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 8; Length 1040;

Best Local Similarity 100.0%; Pred. No. 3.7e-261;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAATACCTCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60

Db 1 ATGCTGGCCACAATACCTCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60

QY 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGTCATTTCCATTCTTTTC 120

Db 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGTCATTTCCATTCTTTTC 120

QY 121 CTCCTGTGAAATGAACACCCGGTCAGTGACCACCAATGGCGGTCAATACTGGTGGTG 180

Db 121 CTCCTGTGAAATGAACACCCGGTCAGTGACCACCAATGGCGGTCAATACTGGTGGTG 180

QY 181 GTCCACAGCGTTTTCTGCTGACAGTGCCTATTCGCTTGACCTACCTCATCAAGAACT 240

Db 181 GTCCACAGCGTTTTCTGCTGACAGTGCCTATTCGCTTGACCTACCTCATCAAGAACT 240

QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTSCCAATGTCACATCCACATGTAC 300

Db 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTSCCAATGTCACATCCACATGTAC 300

QY 301 CTCAGTTCCTATTCTATGTGGTGATCCTCGTCCACAGATACCTCATCTTCTTCAAGTGC 360

Db 301 CTCAGTTCCTATTCTATGTGGTGATCCTCGTCCACAGATACCTCATCTTCTTCAAGTGC 360

QY 361 AAACACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCATGTGG 420

Db 361 AAACACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCATGTGG 420

QY 421 ACGCTGTGATGTTCATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480

Db 421 ACGCTGTGATGTTCATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480

QY 481 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 540

Db 481 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 540

QY 541 ATCAACTATATGATGATCATTTTGTGCATAGCCGTGTCTGTGATTCGTGGTCTTCCAG 600

Db 541 ATCAACTATATGATGATCATTTTGTGCATAGCCGTGTCTGTGATTCGTGGTCTTCCAG 600

QY 601 GTCTTCATCATATTATGTTGATGTCGAGAAGCTACGCCACTCTTTACTATCCACCCAGGAG 660

Db 601 GTCTTCATCATATTATGTTGATGTCGAGAAGCTACGCCACTCTTTACTATCCACCCAGGAG 660

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTCACTCTTGTGTTTCTTCTCC 720

Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTCACTCTTGTGTTTCTTCTCC 720

QY 721 TACAGTCTTTAGGATCTATTACTGAAATGTTGTGACGCAATTCATGCTGTAAACAGC 780

Db 721 TACAGTCTTTAGGATCTATTACTGAAATGTTGTGACGCAATTCATGCTGTAAACAGC 780



```
Db 1 ATGCGTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Qy 61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGGTGATTCATTTCCATCTTTTC 120
Db 61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGGTGATTCATTTCCATCTTTTC 120
Qy 121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTGGTGGTG 180
Db 121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTGGTGGTG 180
Qy 181 GTCACAGCGTTTTCTGCTGACAGTGCAATTCCTGCTGACCTACCTCATCAAGAAGACT 240
Db 181 GTCACAGCGTTTTCTGCTGACAGTGCAATTCCTGCTGACCTACCTCATCAAGAAGACT 240
Qy 241 TGGATGTTGGCTGCCCTCTGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300
Db 241 TGGATGTTGGCTGCCCTCTGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300
Qy 301 CTCAGCTTCTTATCTATGCTGATCTCTGCTGACAGATACCTCATCTTCTCAAGTGC 360
Db 301 CTCAGCTTCTTATCTATGCTGATCTCTGCTGACAGATACCTCATCTTCTCAAGTGC 360
Qy 361 AAAGACAAGTGAATCTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 AAAGACAAGTGAATCTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 ACGCTGGTGAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 ACGCTGGTGAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 TACAATGAGGAGCACTGTTTAAATTCACAAAGCTGCTTACACATGATGGAATC 540
Db 481 TACAATGAGGAGCACTGTTTAAATTCACAAAGCTGCTTACACATGATGGAATC 540
Qy 541 ATCAACTATGATAGTCAATTTTCTGATAGCGTGTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 ATCAACTATGATAGTCAATTTTCTGATAGCGTGTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 GCTTTCATCATATGCTGATGCTGAGAGCTGAGAGCTGCTTACTATCCACAGAG 660
Db 601 GCTTTCATCATATGCTGATGCTGAGAGCTGAGAGCTGCTTACTATCCACAGAG 660
Qy 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTGTTGTTGTTGTTG 720
Db 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTGTTGTTGTTGTTG 720
Qy 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAACAGC 780
Db 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAACAGC 780
Qy 781 AAGTTGCAATTTATAACGAATCTCTTGTAGTGTAAAGCAATTAAGTGTGATTTG 840
Db 781 AAGTTGCAATTTATAACGAATCTCTTGTAGTGTAAAGCAATTAAGTGTGATTTG 840
Qy 841 CTCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 841 CTCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Qy 901 TGTGTTTGGCGGTAG 918
Db 901 TGTGTTTGGCGGTAG 918
```

## RESULT 3

ID ABT04867 standard; cDNA; 918 BP.

XX AC

XX ABT04867;

XX DT

XX 11-OCT-2002 (first entry)

XX Human G protein coupled receptor hrUP29 coding sequence.

XX

Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;  
hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37; gene; ss.  
Homo sapiens.  
WO200242461-A2.

30-MAY-2002.  
26-NOV-2001; 2001WO-US044386.

27-NOV-2000; 2000US-0253404P.  
12-DEC-2000; 2000US-0255366P.  
20-FEB-2001; 2001US-0270266P.  
20-FEB-2001; 2001US-0270286P.  
06-APR-2001; 2001US-0282032P.  
06-APR-2001; 2001US-0282356P.  
06-APR-2001; 2001US-0282358P.  
06-APR-2001; 2001US-0282365P.  
14-MAY-2001; 2001US-0290917P.  
31-JUL-2001; 2001US-0309208P.

(AREN-) ARENA PHARM INC.

Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

WPI; 2002-566565/60.

P-PSDB; ABJ04069.

Novel endogenous and non-endogenous versions of G protein-coupled  
receptor useful for identification of candidate compounds as receptor  
agonists or antagonists for use as therapeutic agents.

Claim 7; Page 56-57; 84pp; English.

The present invention provides the protein and coding sequences of  
several human G-protein coupled receptors (GPCRs). These can be used in  
the identification of candidate compounds as receptor agonists or inverse  
agonists having applicability as therapeutic agents. The present sequence  
is a GPCR coding sequence of the invention

Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;

Best Local Similarity 100.0%; Pred. No. 3.5e-261;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCGTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

1 ATGCGTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

61 ATCAGCCTCTACTTCATAGTGTATTGGCGGCTGGTGGGTGATTCATTTCCATCTTTTC 120

61 ATCAGCCTCTACTTCATAGTGTATTGGCGGCTGGTGGGTGATTCATTTCCATCTTTTC 120

121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTGGTGGTG 180

121 CTCCTGGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTGGTGGTG 180

181 GTCACAGCGTTTTCTGCTGACAGTGCCATTTGCTTGCACCTACCTCATCAAGAAGACT 240

181 GTCACAGCGTTTTCTGCTGACAGTGCCATTTGCTTGCACCTACCTCATCAAGAAGACT 240

241 TGGATGTTGGCTGCCCTCTGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300

241 TGGATGTTGGCTGCCCTCTGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300

301 CTCAGCTTCTTATCTATGCTGATCTCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360

301 CTCAGCTTCTTATCTATGCTGATCTCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360

361 AAAGACAAGTGAATCTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

|||||



CC The present invention provides the protein and coding sequences of a  
CC novel human testis-originated G protein-coupled receptor protein TGR10.  
CC The sequences can be used in the development of drugs for the treatment  
CC of diseases of the central nervous system, inflammations, diseases of the  
CC circulatory system, cancer, metabolic diseases, immunological diseases,  
CC and diseases of the gastrointestinal system. The present sequence is the  
CC coding sequence of the invention  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 918; DB 6; Length 918;  
Best Local Similarity 100.0%; Pred. No. 3.5e-261;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA 60  
DB 1 ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA 60  
  
QY 61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGTGGTGTGTCATTTCCTTTTC 120  
DB 61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGTGGTGTGTCATTTCCTTTTC 120  
  
QY 121 CTCCTGTGTAATGAACACCCGTCAGTCAGTACACCAATGGCGTCAATTAATGTTGGTG 180  
DB 121 CTCCTGTGTAATGAACACCCGTCAGTCAGTACACCAATGGCGTCAATTAATGTTGGTG 180  
  
QY 181 GTCCACAGCGTTTTCCTGCTGACAGTGCCTTTTCGTTGACCTACCTCATCAAGAGACT 240  
DB 181 GTCCACAGCGTTTTCCTGCTGACAGTGCCTTTTCGTTGACCTACCTCATCAAGAGACT 240  
  
QY 241 TGGATGTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCCATGTCGACATCCCATGTAC 300  
DB 241 TGGATGTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCCATGTCGACATCCCATGTAC 300  
  
QY 301 CTCACGTTCTTATCTATGTTGGTGCATCTGTCACCAAGATACCTCATCTTCTCAAGTGC 360  
DB 301 CTCACGTTCTTATCTATGTTGGTGCATCTGTCACCAAGATACCTCATCTTCTCAAGTGC 360  
  
QY 361 AAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCGTGCAGTGTGTCATGTG 420  
DB 361 AAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGCTGCGTGCAGTGTGTCATGTG 420  
  
QY 421 ACGTGTGTATGTCATGTTGGTACCTGCTGTCACCGGTATGGAATCCATGAGGAA 480  
DB 421 ACGTGTGTATGTCATGTTGGTACCTGCTGTCACCGGTATGGAATCCATGAGGAA 480  
  
QY 481 TACAATGAGGAGCACTGTTTAAATTTCAAGAGCTTCTTACACATATGTGAATAATC 540  
DB 481 TACAATGAGGAGCACTGTTTAAATTTCAAGAGCTTCTTACACATATGTGAATAATC 540  
  
QY 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGATTCGTTGGTCTTCCAG 600  
DB 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGATTCGTTGGTCTTCCAG 600  
  
QY 601 GTCTTCATCATATGTTGTCAGAGCTACGCCACTCTTTACTATCCCAACAGGAG 660  
DB 601 GTCTTCATCATATGTTGTCAGAGCTACGCCACTCTTTACTATCCCAACAGGAG 660  
  
QY 661 TCTGGGCTCAGTGAAACCACTTTTATAGGGGTCTCCTGTTGTTCTTCTTCC 720  
DB 661 TCTGGGCTCAGTGAAACCACTTTTATAGGGGTCTCCTGTTGTTCTTCTTCC 720  
  
QY 721 TACCAGTCTTTAGGATCTATTCTGAATGTTGTAGCGATTCCTCAATGCTGTAAACAG 780  
DB 721 TACCAGTCTTTAGGATCTATTCTGAATGTTGTAGCGATTCCTCAATGCTGTAAACAG 780  
  
QY 781 AAGTTGCATTTTATACGAATCTTCTGAGTGTAACAGCAATTAGCTCTATGATTG 840  
DB 781 AAGTTGCATTTTATACGAATCTTCTGAGTGTAACAGCAATTAGCTCTATGATTG 840  
  
QY 841 CTTCCTCTTCTTGGGGAGGCAATTTGTTTAAAGCAAGATAATTTGGCTTATGGAAT 900  
DB 841 CTTCCTCTTCTTGGGGAGGCAATTTGTTTAAAGCAAGATAATTTGGCTTATGGAAT 900

QY 901 TGTGTTTGTGCGGTAG 918  
DB 901 TGTGTTTGTGCGGTAG 918

RESULT 2

ABA00160  
ID ABA00160 standard; cDNA; 918 BP.

XX ABA00160;

XX 15-NOV-2002 (first entry)

XX PFI-021 cDNA.

XX Genes; human; G-protein coupled receptor; GPCR; PFI-021;  
KW peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;  
KW respiratory; neurology; psychology; urogenital disease;  
KW reproductive dysfunction; sexual dysfunction; cancer; tissue repair;  
KW dermatology; skin pigmentation; photoaging; frailty; osteoporosis;  
KW metabolic disease; cardiovascular disease; sleep disorder; hair loss;  
KW gastrointestinal disease; anti-infection; sensory organ disorder; ss.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH 1..918  
CDS /\*tag= a  
FT /\*product= "PFI-021"

XX EPI225183-A2.

XX 24-JUL-2002.

XX 09-JAN-2002; 2002EP-00250128.

XX 23-JAN-2001; 2001GB-00001739.

XX (PFIZ ) PFIZER LTD.

XX (PFIZ ) PFIZER INC.

XX Harland L;

XX WPI; 2002-601226/65.

XX P-PSDB; AAG79446.

XX New human G-protein coupled receptor involved in signal transduction,  
PT useful to treat disorders associated with its expression or activity such  
PT as inflammation, allergy and cancer.

XX Claim 1; Fig 1; 8pp; English.

XX This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.  
CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA  
CC libraries from peripheral blood mononuclear cells. Two ESTs have been  
CC identified in libraries derived from breast mRNA. PFI-021 and the  
CC corresponding cDNA are used to treat a patient needing altered activation  
CC or expression of a GPCR, such as inflammation, allergy and respiratory,  
CC neurology, psychology, urogenital disease, reproductive and sexual  
CC dysfunction/disorders, cancer, tissue repair, dermatology, skin  
CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic  
CC disease, cardiovascular disease, gastro-intestinal disease, anti-  
CC infection, sensory organ disorders, sleep disorders and hair loss  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;  
Best Local Similarity 100.0%; Pred. No. 3.5e-261;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA 60  
|||||

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 09:09:59 ; Search time 451 Seconds

(without alignments)  
8647.108 Million cell updates/sec

Title: US-10-055-106c-1

Perfect score: 918

Sequence: 1 atgctggcccaataacctc.....attgtgttttgcgcgttag 918

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6	AAL44713 Human tes
2	918	100.0	918	6	ABA00160
3	918	100.0	918	6	ABT04867 Human G p
4	918	100.0	918	7	ABZ59171 Human TGR
5	918	100.0	1040	8	AAL57070 Human G-p
6	918	100.0	1336	6	Aaf88583 Human GCR
7	918	100.0	1340	6	Aaf88584 Human GCR
8	918	100.0	1460	6	Aaf88585 Human GCR
9	918	100.0	2525	4	AaH51009 Human ncp
10	918	100.0	2525	4	ABH570242 DNA encod
11	918	100.0	113306	9	ADCB6554 Human GPC
12	916.4	99.8	1051	6	ABX87351 Human cDN
13	916.4	99.8	1684	6	AAL53413 1684 nt c
14	913.4	99.5	939	6	AAL53414 939 nt co
15	895	97.5	1499	6	AAD37670 Human G-p
16	890	75.2	372	9	ADCL2789 Human GPC
17	560.8	61.1	810	9	ADB78584 Mouse g-p
18	390	42.5	447	4	AaH50979 Human ncp
19	390	42.5	447	6	ABH70212 DNA encod
20	162	17.6	479	4	AaK56763 Human lmm
21	144.8	15.8	897	7	ABZ23663 G protein
22	76.4	8.3	1113	5	AB198010 Non-endog
23	76.4	8.3	1805	6	ABH53446 CDNA enco

#### ALIGNMENTS

##### RESULT 1

AAL44713

ID AAL44713 standard; DNA; 918 BP.

AC AAL44713;

DT 03-MAY-2002 (first entry)

Human testis originated G-protein coupled receptor TGR10 coding sequence.

Human; testis-originated G-protein coupled receptor; TGR10; inflammatory; cytosolic; immunomodulator; cardiac; neuroprotective; gene therapy; inflammation; nervous system disease; circulatory system disease; cancer; metabolic disease; immunological disease; gastrointestinal disease; gene; ds.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS i. 918

FT /tag= a

FT /product= "TGR10"

XX WO200196567-A1.

XX PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-JP005061.

XX PR 15-JUN-2000; 2000JP-00184596.

XX PR 19-JUL-2000; 2000JP-00223887.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Moriya T, Ito T, Shintani Y, Miyajima N;

XX WPI; 2002-098071/13.

XX P-PSDB; AAM48989.

Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat e.g. diseases of central nervous system, inflammations and diseases of circulatory system.

XX Claim 5; Page 99; 110pp; Japanese.

XX

Abx94264 Human orp  
Abx94262 Human orp  
Abx94263 Human orp  
Aca56793 Human sig  
Adc40517 DNA deriv  
Abx94045 CDNA enco  
Abz42709 Human orp  
Abx94260 Human orp  
Aaz60659 DNA encod  
Aaz60658 DNA encod  
Abx94254 Human orp  
Abx94261 Human orp  
Abi98011 Non-endog  
Aca56819 Human sig  
Abz42678 Human orp  
Aad58490 Human kap  
Ade84861 Farnesyl  
Abx94042 Rat orpha  
Aaq75928 Mouse opl  
Abx94039 Rat orpha  
Aaq89233 Rat oplol  
Aaa59510 CDNA enco

24 76.4 8.3 1829 7 ABX94264  
25 76.4 8.3 1829 7 ABX94262  
26 76.4 8.3 1829 7 ABX94263  
27 76.4 8.3 1973 7 ACA56793  
28 76.4 8.3 1973 9 ADC40517  
29 76.4 8.3 2534 7 ABX94045  
30 76.4 8.3 2534 7 ABZ42709  
31 74.8 8.1 1829 7 ABX94260  
32 73.2 7.6 1134 3 AAZ60659  
33 70.2 7.6 1177 3 AAZ60658  
34 69.6 7.6 2602 7 ABX94254  
35 68 7.4 1947 7 ABX94261  
36 61 6.6 1143 5 ABI98011  
37 61 6.6 1182 7 ACA56819  
38 61 6.6 1182 7 ABZ42678  
39 61 6.6 1182 9 AAD58490  
40 61 6.6 1182 9 ADE84861  
41 59.8 6.5 1243 7 ABX94042  
42 59.8 6.5 1330 2 Aaq75928  
43 59.8 6.5 1387 7 ABX94039  
44 59.8 6.5 1567 2 Aaq89233  
45 59.8 6.5 1567 3 Aaa59510

XX 28-FEB-2002; 2002MO-US006455.  
XX 01-MAR-2001; 2001US-0272677P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Glucksmann MA;  
XX WPI; 2002-732793/79.  
XX P-PSDB; AAO22919.  
XX New G-protein coupled receptor used in receptor assays as a target for  
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and  
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism  
PT disorders.  
XX Claim 5; Page 101-103; 105pp; English.  
XX The invention relates to an isolated polypeptide, which is a G-protein  
CC coupled receptor (GPCR) related to subfamily I of G-protein coupled  
CC receptor type proteins (GPCRs), designated the 93870 receptor. The  
CC polypeptides, nucleic acid molecules and antibodies of the invention are  
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
CC monitoring clinical trials or pharmacogenetics), or in methods of  
CC treatment (e.g. therapeutic and prophylactic). They are useful in  
CC treating and diagnosing conditions related to aberrant activity or  
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and  
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism  
CC disorders, or bone marrow mononuclear disorders, as well as cellular  
CC proliferative and/or differentiative disorders, hormonal disorders,  
CC neurological disorders, cardiovascular disorders, viral diseases, liver  
CC disorders, and pain and metabolic disorders. Conditions that can be  
CC treated include cancer, diabetes mellitus, hypothyroidism,  
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or  
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,  
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,  
CC Huntington's disease, heart failure, angina pectoris, myocardial  
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,  
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host  
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The  
CC transgenic animals are useful for studying the function and/or activity  
CC of a 93870 protein and for identifying and/or evaluating modulators of  
CC 93870 activities. The polynucleotides of the invention can be used in  
CC gene therapy. This polynucleotide sequence represents the 939 nucleotide  
CC DNA of the human G-protein coupled receptor type protein of the invention  
XX  
SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;

Query Match 94.1%; Score 864; DB 6; Length 939;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGTGGCCACAATACCTCCAGGATTCCTCTTGGGATCCTATAGTGACACCCACCTTA 60  
DB |||||||  
QY 25 ATGCGTGGCCACAATACCTCCAGGATTCCTCTTGGGATCCTATAGTGACACCCACCTTA 84  
DB |||||||  
QY 61 ATCAGCGCTCTACTTCATAGTGTCTTATTTGGCGGGCTGGTGGGTGTCATTTCCATTCTTTTC 120  
DB |||||||  
QY 85 ATCAGCGCTCTACTTCATAGTGTCTTATTTGGCGGGCTGGTGGGTGTCATTTCCATTCTTTTC 144  
DB |||||||  
QY 121 CTCCTGGTGAAAATGAAACCCGGTCAGTGACACCAATGGCGGTGATTAACCTTGGTGGTG 180  
DB |||||||  
QY 145 CTCCTGGTGAAAATGAAACCCGGTCAGTGACACCAATGGCGGTGATTAACCTTGGTGGTG 204  
DB |||||||  
QY 181 GTCCACAGCGTTTTCTGTGTGACAGTGCCATTTGCTGTGACCTCTCATCAAGAGACT 240  
DB |||||||  
QY 205 GTCCACAGCGTTTTCTGTGTGACAGTGCCATTTGCTGTGACCTCTCATCAAGAGACT 264  
DB |||||||  
QY 241 TGGATGTTTGGCGTGCCTCTCTGCAAAATTTGTAGTGCCATGCTGCACATGCATGTAC 300  
DB |||||||  
QY 265 TGGATGTTTGGCGTGCCTCTCTGCAAAATTTGTAGTGCCATGCTGCACATGCATGTAC 324  
DB |||||||

QY 301 CTCACGTTCCCTATTCTATGTGGTGATCCTGGTCCACAGATACCTCATCTCTTCTCAAGTGC 360  
DB |||||||  
QY 325 CTCACGTTCCCTATTCTATGTGGTGATCCTGGTCCACAGATACCTCATCTCTTCTCAAGTGC 384  
DB |||||||  
QY 361 AAGACAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 420  
DB |||||||  
QY 385 AAGACAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 444  
DB |||||||  
QY 421 ACGCTGGTGAATTCATTGTGGTACCCCTGGTGTCTCCCGGTATGGAAATCCATAGGAA 480  
DB |||||||  
QY 445 ACGCTGGTGAATTCATTGTGGTACCCCTGGTGTCTCCCGGTATGGAAATCCATAGGAA 504  
DB |||||||  
QY 481 TACAAATGAGGACACTGTTTTTAAATTTCAAAAGAGCTTGCCTTACATATGTGAAATC 540  
DB |||||||  
QY 505 TACAAATGAGGACACTGTTTTTAAATTTCAAAAGAGCTTGCCTTACATATGTGAAATC 564  
DB |||||||  
QY 541 ATCAACTATATGATAGTAGTCAATTTTGTGATAGCGGTGTCTGTGATTTCTGTGGTCTTCCAG 600  
DB |||||||  
QY 565 ATCAACTATATGATAGTAGTCAATTTTGTGATAGCGGTGTCTGTGATTTCTGTGGTCTTCCAG 624  
DB |||||||  
QY 601 GTCTTCATCATATTATGTGTGATGGTGCAGAACTAGCCACTCTTTACTATCCACCAGGAG 660  
DB |||||||  
QY 625 GTCTTCATCATATTATGTGTGATGGTGCAGAACTAGCCACTCTTTACTATCCACCAGGAG 684  
DB |||||||  
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTTGTGTGTTTCTTCCC 720  
DB |||||||  
QY 685 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTTGTGTGTTTCTTCCC 744  
DB |||||||  
QY 721 TACAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 780  
DB |||||||  
QY 745 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAGCAGC 804  
DB |||||||  
QY 781 AAGGTTGCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTGATGTTG 840  
DB |||||||  
QY 805 AAGGTTGCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTGATGTTG 864  
DB |||||||  
QY 841 CTCTCTTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATPAATTTGGCTTATGGAAT 900  
DB |||||||  
QY 865 CTCTCTTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATPAATTTGGCTTATGGAAT 924  
DB |||||||  
QY 901 TGTGTTTTTGTGCGGT 915  
DB |||||||  
QY 925 TGTGTTTTTGTGCGGT 939  
DB |||||||

Search completed: April 25, 2004, 18:01:46  
Job time : 454 secs

XX PS Claim 5; Page 99-100; 105pp; English.

XX CC The invention relates to an isolated polypeptide, which is a G-protein

CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled

CC receptor type proteins (GPCRs), designated the 93870 receptor. The

CC polypeptides, nucleic acid molecules and antibodies of the invention are

CC useful in screening assays, predictive medicine (e.g. diagnostic assays,

CC monitoring clinical trials or pharmacogenetics), or in methods of

CC treatment (e.g. therapeutic and prophylactic). They are useful in

CC treating and diagnosing conditions related to aberrant activity or

CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and

CC inflammatory disorders, platelet disorders, skeletal or bone metabolism

CC disorders, or bone marrow mononuclear disorders, as well as cellular

CC proliferative and/or differentiative disorders, hormonal disorders,

CC neurological disorders, cardiovascular disorders, viral diseases, liver

CC disorders, and pain and metabolic disorders. Conditions that can be

CC treated include cancer, diabetes mellitus, hypothyroidism,

CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or

CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,

CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,

CC Huntington's disease, heart failure, angina pectoris, myocardial

CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,

CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host

CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The

CC transgenic animals are useful for studying the function and/or activity

CC of a 93870 protein and for identifying and/or evaluating modulators of

CC 93870 activities. The polynucleotides of the invention can be used in

CC gene therapy. This polynucleotide sequence represents the cDNA of the

CC 1684 nucleotide human G-protein coupled receptor type protein of the

XX CC invention

XX SQ Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;

Query Match 94.4%; Score 867; DB 6; Length 1684;

Best Local Similarity 99.94; Pred. No. 0;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60

DB 171 ATGCTTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 230

QY 61 ATGAGCTCTACTTCAATGCTTATTTGGGGCTGGTGGTGCATTTCCATCTTTTC 120

DB 231 ATGAGCTCTACTTCAATGCTTATTTGGGGCTGGTGGTGCATTTCCATCTTTTC 290

QY 121 CTCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTCAATTAACCTGGTGGTG 180

DB 291 CTCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTCAATTAACCTGGTGGTG 350

QY 181 GTCCACAGCGTTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 240

DB 351 GTCCACAGCGTTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 410

QY 241 TGGATGTTGGGCTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300

DB 411 TGGATGTTGGGCTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 470

QY 301 CTCACGTTCTCTATTCTATGTTGGTATCCTGGTCAACAGATPACCTCATCTTTCTCAAGTGC 360

DB 471 CTCACGTTCTCTATTCTATGTTGGTATCCTGGTCAACAGATPACCTCATCTTTCTCAAGTGC 530

QY 361 AAGACAAAGTGGAAATCTACAGAAATCTCATGCTGTGGCTGCCAGTGGCATGTGG 420

DB 531 AAGACAAAGTGGAAATCTACAGAAATCTCATGCTGTGGCTGCCAGTGGCATGTGG 590

QY 421 ACGTGTGTGATGTCAATTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGAA 480

DB 591 ACGTGTGTGATGTCAATTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGAA 650

QY 481 TACAATCAGAGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAATC 540

DB 651 TACAATCAGAGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAATC 710

QY 541 ATCAACTATATGATAGTCAATTTTTTGTCTATAGCCGTTCTGCTGATCTCTGTTGTTCCAG 600

DB 711 ATCAACTATATGATAGTCAATTTTTTGTCTATAGCCGTTCTGCTGATCTCTGTTGTTCCAG 770

QY 601 GTCTTTCATCATTTATGTTGATGTCGACAGAGCTAGCCCACTCTTTACTATATCCCAAGGAG 660

DB 771 GTCTTTCATCATTTATGTTGATGTCGACAGAGCTAGCCCACTCTTTACTATATCCCAAGGAG 830

QY 661 TTTGGGGCTAGCTGAAACCAATTTTTTATAGGGGTCACTCTTTGTTTCTTCTTCCC 720

DB 831 TTTGGGGCTAGCTGAAACCAATTTTTTATAGGGGTCACTCTTTGTTTCTTCTTCCC 890

QY 721 TACCAGTTCTTTAGGACTATTTACTGAAATGTTCTGACGCAATTCCTCAATGCTGTAAACAGC 780

DB 891 TACCAGTTCTTTAGGACTATTTACTGAAATGTTCTGACGCAATTCCTCAATGCTGTAAACAGC 950

QY 781 AAGGTTGCATTTTAAACGAAATCTTTCTGAGTGAACAGCAATAGCTGCTATGATTTG 840

DB 951 AAGGTTGCATTTTAAACGAAATCTTTCTGAGTGAACAGCAATAGCTGCTATGATTTG 1010

QY 841 CTCTCTCTTGTCTTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900

DB 1011 CTCTCTCTTGTCTTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1070

QY 901 TGTGTTTGTGCGGTAG 918

DB 1071 TGTGTTTGTGCGGTAG 1088

RESULT 15

AAL53414

ID AAL53414 standard; DNA; 939 BP.

XX AC AAL53414;

XX DT 12-DEC-2002 (first entry)

XX DE 939 nt coding DNA of a human G-protein coupled receptor type protein.

KW Anti-HIV; cytostatic; antidiabetic; antilasthmatic; antiinflammatory;

KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;

KW antibacterial; virocidic; fungicide; analgesic; antiparkinsonian; GPCR;

KW cardiant; dermatological; antiinfertility; hepatotropic; antiallergic;

KW antipsoriatic; ophthalmologic; antitubercular; antihypertensive; anticonvulsant;

KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;

KW 93870 receptor; immune; inflammatory disorder; bone marrow mononuclear disorder;

KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;

KW cellular proliferative; differentiative disorder; viral disease; pain;

KW neurological disorder; cardiovascular disorder; cancer; diabetes mellitus; bacterial;

KW liver disorder; metabolic disorder; hyperthyroidism; reproductive; fertility disorder; HIV;

KW hypothyroidism; fungal meningoencephalitis; multiple sclerosis;

KW viral meningitis; Parkinson's disease; ataxia-telangiectasia;

KW Huntington's disease; heart failure; angina pectoris; dermatitis;

KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;

KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;

KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;

KW transgenic animal; human; gene; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT 1. 939

FT CDS /tag= a

FT /partial

FT /product= "Human G-protein coupled receptor type protein

FT 93870"

FT /note= "No stop codon"

XX WO200270657-A2.

XX 12-SEP-2002.

CC derived from the cell, an antibody immunospecific for IGS70. IGS70 is  
CC useful for diagnosing a disease or a susceptibility to disease in a  
CC subject related to expression or activity of the IGS70 polypeptide in a  
CC subject by determining the presence or absence of mutation in the  
CC nucleotide sequence encoding IGS70 in the genome of the subject in a  
CC sample derived from the subject. IGS70 is also useful identifying agonist  
CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified  
CC ant/agonists are useful for treating psychiatric and central nervous  
CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,  
CC multiple sclerosis, anxiety, cardiovascular diseases such as heart  
CC failure, angina pectoris, myocardial infarction, kidney disease such as  
CC renal failure, gastrointestinal disorders such as irritable bowel  
CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,  
CC inflammation, cancers, asthma, infection (such as bacterial, viral,  
CC fungal, protozoal) especially human immunodeficiency virus infection  
CC (HIV), diabetes, osteoporosis and allergies. The present sequence encodes  
CC the human GPCR IGS70  
XX

Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 94.4%; Score 867; DB 6; Length 1051;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGTGGCCACATACCTCCAGGAATTCCTTCGCGATCCTATAGTCACACCCACCTTA 60  
Db 60 ATGCGTGGCCACATACCTCCAGGAATTCCTTCGCGATCCTATAGTCACACCCACCTTA 119  
QY 61 ATCAGCCTCTACTTCATAGTGGTATTTGGCGGCTGGTGGTGTCTATTCCTATTCCTTC 120  
Db 120 ATCAGCCTCTACTTCATAGTGGTATTTGGCGGCTGGTGGTGTCTATTCCTATTCCTTC 179  
QY 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGGTCAATTAACCTGGTGTG 180  
Db 180 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGGTCAATTAACCTGGTGTG 239  
QY 181 GTCCACAGGTTTCTGCTGACGTGCATTCCTGCTGACCTACTCTATCAGAGACT 240  
Db 240 GTCCACAGGTTTCTGCTGACGTGCATTCCTGCTGACCTACTCTATCAGAGACT 299  
QY 241 TGGATGTTTGGCTGCCCTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGATGAC 300  
Db 300 TGGATGTTTGGCTGCCCTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGATGAC 359  
QY 301 CTCAGTTCCTATTCATGTGTGTGATCCTGTCACAGATACCTATCTTCTCAAGTGC 360  
Db 360 CTCAGTTCCTATTCATGTGTGTGATCCTGTCACAGATACCTATCTTCTCAAGTGC 419  
QY 361 AAAGACAAAGTGAATTTACAGAAATTCGATGCTGGCTGCCAGTGGCATGTGG 420  
Db 420 AAAGACAAAGTGAATTTACAGAAATTCGATGCTGGCTGCCAGTGGCATGTGG 479  
QY 421 AGCTGGTGATGTGATGTGTGATCCCTGGTGTGTCCTCCGGTATGGAATCCATGAGAA 480  
Db 480 AGCTGGTGATGTGATGTGTGATCCCTGGTGTGTCCTCCGGTATGGAATCCATGAGAA 539  
QY 481 TACATGAGGACACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540  
Db 540 TACATGAGGACACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 599  
QY 541 ATCAACTATATGATAGTCATTTTGTGATGCGGTGTGCTGATTCGTGCTTCACG 600  
Db 600 ATCAACTATATGATAGTCATTTTGTGATGCGGTGTGCTGATTCGTGCTTCACG 659  
QY 601 GTCTTCATCATTTATGTTGATGTCGAGAGCTACCGACTCTTTACTATCCACAGAG 660  
Db 660 GTCTTCATCATTTATGTTGATGTCGAGAGCTACCGACTCTTTACTATCCACAGAG 719  
QY 661 TTCTGGGTGCTGAGTGAACCACTATTTTATAGGGGTGATCCTTGTGTTTGTTCCTCC 720  
Db 720 TTCTGGGTGCTGAGTGAACCACTATTTTATAGGGGTGATCCTTGTGTTTGTTCCTCC 779  
QY 721 TACCAGTCTTTAGGATCTATTAATGATGTTGTGACGCAATCCCAATGCTGTAAACAGC 780

Db 780 TACAGTCTTTAGGATCTATTAATGTTGTGACCAATCCATGCTGTAAACAGC 839  
QY 781 AAGTTGCAATTTATTAACGAATCTCTTCTGAGTGTAAACGAATTAAGTCTGTATGTTG 840  
Db 840 AAGTTGCAATTTATTAACGAATCTCTTCTGAGTGTAAACGAATTAAGTCTGTATGTTG 899  
QY 841 CTCTCTCTCTCTCTCTTGGGGGAAGCCATTTGTTTAAACAAAGATTAATTTGCTTATGGAAT 900  
Db 900 CTCTCTCTCTCTCTTGGGGGAAGCCATTTGTTTAAACAAAGATTAATTTGCTTATGGAAT 959  
QY 901 TGTGTTTGTGCGCTTAG 918  
Db 960 TGTGTTTGTGCGCTTAG 977

RESULT 14

AAL53413

ID AAL53413 standard; cDNA; 1684 BP.

XX AAL53413;

XX 12-DEC-2002 (first entry)

XX 1684 nt cDNA of human G-protein coupled receptor type protein.

XX Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;  
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;  
XX antibiotic; virucide; fungicide; analgesic; antiparkinsonian; GPCR;  
XX cardiac; dermatological; antifertility; hepatotropic; antiallergic;  
XX antipariatic; ophthalmological; antianginal; antithyroid; anticonvulsant;  
XX antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;  
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;  
XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;  
XX cellular proliferative; differentiative disorder; hormonal disorder;  
XX neurological disorder; cardiovascular disorder; viral disease; pain;  
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;  
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;  
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;  
XX Huntington's disease; heart failure; angina pectoris; dermatitis;  
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;  
XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;  
XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;  
XX transgenic animal; human; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 147..1088

XX FT /\*tag= a

XX FT /product= "Human G-protein coupled receptor type protein

XX 93870"

XX WO200270657-A2.

XX 12-SEP-2002.

XX 28-FEB-2002; 2002WO-US0006455.

XX 01-MAR-2001; 2001US-0272677P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA;

XX WPI; 2002-732793/79.

XX DR P-PSDB; AAO22919.

XX New G-protein coupled receptor used in receptor assays as a target for

XX diagnosis and treatment of receptor-mediated disorders, e.g. immune and

XX inflammatory disorders, platelet disorders, skeletal or bone metabolism

XX disorders.

PI Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;  
XX WPI; 2002-426012/45.  
DR P-PSDB; AAE23414.  
XX Novel G-protein coupled receptor polypeptides referred as GCREC peptides,  
PT useful for treating multiple sclerosis, cholecystitis heart failure,  
PT angina pectoris, rheumatoid arthritis, obesity, osteoporosis.  
XX Claim 83; Page 140; 147pp; English.  
XX The invention relates to human G-protein coupled receptor (GCREC 1-16)  
CC polypeptides and polynucleotides. Sequences of the invention are useful  
CC for the diagnosis, treatment and prevention of cell proliferative (e.g.  
CC cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's  
CC disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,  
CC heart failure), gastrointestinal (e.g. anorexia, cholecystitis),  
CC autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)  
CC and metabolic disorders (e.g. obesity, osteoporosis), viral infections,  
CC atherosclerosis and hepatitis. GCREC proteins are useful for identifying  
CC compounds that modulate, mimic and block olfactory and taste sensations.  
CC They are also useful for identifying GCREC modulators. GCREC DNAs are  
CC useful in gene therapy. The present sequence is human GCREC-6 cDNA  
XX SQ Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;  
Query Match 96.6%; Score 887; DB 6; Length 1499;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTGGGCAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 60  
DB 381 ATGCTGGGCAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACCTTA 440  
QY 61 ATCAGGCTCTACTTCTATAGTCTTATTGGGGGCTGGTGGTCTCATTTCCATTCTTTTC 120  
DB 441 ATCAGGCTCTACTTCTATAGTCTTATTGGGGGCTGGTGGTCTCATTTCCATTCTTTTC 500  
QY 121 CTCTCGTGAATAGAACCCCGTCAGTGACACCATCGCGTCAATTAACCTTGGTGTG 180  
DB 501 CTCTCGTGAATAGAACCCCGTCAGTGACACCATCGCGTCAATTAACCTTGGTGTG 560  
QY 181 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTACCTTACCTCATCAAGAGACT 240  
DB 561 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTACCTTACCTCATCAAGAGACT 620  
QY 241 TGGATGTTGGGCTGCCCTTCTCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 300  
DB 621 TGGATGTTGGGCTGCCCTTCTCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 680  
QY 301 CTCACGTTCTTATCTATGTTGATCCCTGGTCAACGATACCTCATCTTCTCAAGTGC 360  
DB 681 CTCACGTTCTTATCTATGTTGATCCCTGGTCAACGATACCTCATCTTCTCAAGTGC 740  
QY 361 AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGTCCAGTCTGGCATGTGG 420  
DB 741 AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGTCCAGTCTGGCATGTGG 800  
QY 421 ACCTGGTGAATTTCTGTTGTTGATCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 480  
DB 801 ACCTGGTGAATTTCTGTTGTTGATCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 860  
QY 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540  
DB 861 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 920  
QY 541 ATCAACTATATGATGATCATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 600  
DB 921 ATCAACTATATGATGATCATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 980  
QY 601 GTCTTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 660  
DB 981 GTCTTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 1040

QY 661 TTCTGGGCTAGCTGAAAAACCTATTTTATAGGGGTACCTGTTGTTTCTTCTTCCC 720  
DB 1041 TTCTGGGCTAGCTGAAAAACCTATTTTATAGGGGTACCTGTTGTTTCTTCTTCCC 1100  
QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 780  
DB 1101 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 1160  
QY 781 AAGTTGCATTTTATAAGAAATCTTCTTGAGTGTACACGAATTAGCTGCTATGATTG 840  
DB 1161 AAGTTGCATTTTATAAGAAATCTTCTTGAGTGTACACGAATTAGCTGCTATGATTG 1220  
QY 841 CTCTCTTTGCTTTTGGGGAAGCAATGCTTTTAAAGCAAAAGATAAT 887  
DB 1221 CTCTCTTTGCTTTTGGGGAAGCAATGCTTTTAAAGCAAAAGATAAT 1267  
RESULT 13  
ABK87351  
ID ABK87351 standard; cDNA; 1051 BP.  
XX AC ABK87351;  
XX DT 24-SEP-2002 (first entry)  
XX Human cDNA encoding G protein-coupled receptor IGS70.  
DE Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS;  
KW psychiatric disorder; central nervous system disorder; schizophrenia;  
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;  
KW heart failure; angina pectoris; myocardial infarction; kidney disease;  
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;  
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;  
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;  
KW osteoporosis; allergy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 60..977  
FT /tag= a  
FT /product= "GPCR IGS70"  
XX WO200244212-A2.  
XX PD 06-JUN-2002.  
XX PF 23-NOV-2001; 2001WO-EP013706.  
XX PR 30-NOV-2000; 2000EP-00204280.  
XX PR 05-DEC-2000; 2000US-0251045P.  
XX PA (SOLV ) SOLVAY PHARM BV.  
XX PI Deleersnijder W, Blockx H, De Moor L;  
XX WPI; 2002-527703/56.  
XX P-PSDB; AAU99179.  
XX Novel G-protein coupled receptor IGS70 polypeptide useful for treating  
PT dysfunctions, disorders or disease related to lung, bone marrow, spinal  
PT cord immune system.  
XX Claim 1; Page 6; 58pp; English.  
XX The invention relates to a G protein-coupled receptor (GPCR) IGS70  
CC polypeptide including sequences that are 98-99.6% identical. Also  
CC included are the polynucleotide encoding IGS70 (including sequences 98-  
CC 99.6% identical to the polynucleotide or the DNA insert contained in  
CC plasmid CBS 109818), a hybridisation probe derived from the  
CC polynucleotide, a DNA or RNA expression system producing IGS70, a host  
CC comprising the expression system, IGS70 receptor membrane preparation

XX 02-JAN-2003.  
XX 18-JUN-2002; 2002EP-00013517.  
XX 18-JUN-2001; 2001JP-00246789.  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
XX Suwa M, Asai K, Akiyama Y, Aburatani H;  
XX WPI; 2003-315783/31.  
XX P-PSDB; ADC86555.  
XX New polynucleotide, useful for preparing a composition for treating a  
XX patient in need of increased or suppressed activity or expression of the  
XX guanosine triphosphate-binding protein coupled receptor.  
XX Claim 1; SEQ ID NO 1007; 28pp; English.  
XX The invention relates to a novel polynucleotide encoding a guanosine  
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
XX the invention may have a use in gene therapy. The polynucleotide and  
XX polypeptide are useful for preparing a composition for treating a patient  
XX in need of increased or suppressed activity or expression of the  
XX guanosine triphosphate-binding protein coupled receptor. The  
XX polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the  
XX invention.  
XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 918; DB 9; Length 113306;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 ATGCTGCGCCAAATACCTCCAGGAATTCCTCTCGATCTATAGTGACACCCACCTTA 60  
XX 11540 ATGCTGCGCCAAATACCTCCAGGAATTCCTCTCGATCTATAGTGACACCCACCTTA 11599  
XX 61 ATGAGCCTCTACTTCATAGTGCTTATTGCGGGCTGGTGGGTGATTCATTCATTCCTTTTC 120  
XX 11600 ATGAGCCTCTACTTCATAGTGCTTATTGCGGGCTGGTGGGTGATTCATTCATTCCTTTTC 11659  
XX 121 CTCCTGGTGAATTAACACCCGGTCAGTGACCCACCATGGGGTCAATTAAGTTGGTGGT 180  
XX 11660 CTCCTGGTGAATTAACACCCGGTCAGTGACCCACCATGGGGTCAATTAAGTTGGTGGT 11719  
XX 181 GTCCACAGCGTTTCTGTCAGAGTGCCATTCCTTGACCTACCTCATCAAGAAGACT 240  
XX 11720 GTCCACAGCGTTTCTGTCAGAGTGCCATTCCTTGACCTACCTCATCAAGAAGACT 11779  
XX 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
XX 11780 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 11839  
XX 301 CTCAGTTCTCTATTCTATGTGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360  
XX 11840 CTCAGTTCTCTATTCTATGTGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 11899  
XX 361 AAAGCAAAAGTGAATTTACAGAAAATGTCATGCTGGTGGCAGTGCTGGCATGTGG 420  
XX 11900 AAAGCAAAAGTGAATTTACAGAAAATGTCATGCTGGTGGCAGTGCTGGCATGTGG 11959  
XX 421 ACGTGGTGATTTGTCATGTTGTATCCCTCGTGTGTCCTCCGGTATGGAATCCATGAGAA 480  
XX 11960 ACGTGGTGATTTGTCATGTTGTATCCCTCGTGTGTCCTCCGGTATGGAATCCATGAGAA 12019  
XX 481 TACATGAGGAGCACTGTTTAAATTTACAAAAGAGCTTGCTTACACATATGTGAAAATC 540  
XX 12020 TACATGAGGAGCACTGTTTAAATTTACAAAAGAGCTTGCTTACACATATGTGAAAATC 12079  
XX 541 ATCAACTATATGATAGTCAATTTTGTGTCATAGCCGTTGCTGTGATCTCTGCTTCCAG 600

Db 12080 ATCAACTATATGATAGTCAATTTTGTGTCATAGCCGTTGCTGTGATCTCTGTTGCTTCCAG 12139  
Qy 601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 660  
Db 12140 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 12199  
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC 720  
Db 12200 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCC 12259  
Qy 721 TACAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCATTCGAATGCCTGTATACAGC 780  
Db 12260 TACAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCATTCGAATGCCTGTATACAGC 12319  
Qy 781 AAGTGTGATTTTATACGAAATCTTTCTTGAGTGTAAAGCAATTAGCTGCTATGATTG 840  
Db 12320 AAGTGTGATTTTATACGAAATCTTTCTTGAGTGTAAAGCAATTAGCTGCTATGATTG 12379  
Qy 841 CTCTCTCTTGTCTTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTCGCTTATGGAAT 900  
Db 12380 CTCTCTCTTGTCTTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTCGCTTATGGAAT 12439  
Qy 901 TGTGTTTGTGCGCTTAG 918  
Db 12440 TGTGTTTGTGCGCTTAG 12457  
RESULT 12  
AAD37670  
ID AAD37670 standard; cDNA; 1499 BP.  
XX  
AC AAD37670;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human G-protein coupled receptor-6 (GCRC-6) cDNA.  
XX  
KW Human; G-protein coupled receptor-6; GCRC-6; atherosclerosis; cancer;  
KW cell proliferative disorder; gastrointestinal; autoimmune; metabolic;  
KW neurological; inflammatory; cardiovascular; viral infection; anorexia;  
KW cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;  
KW Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;  
KW rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;  
KW osteoporosis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 381..1400  
FT /tag= a  
FT /product= "Human GCRC-6 protein"  
XX  
FN WO200226825-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 28-SEP-2001; 2001WO-US030661.  
XX  
PR 29-SEP-2000; 2000US-0236546P.  
PR 13-OCT-2000; 2000US-0240589P.  
PR 20-OCT-2000; 2000US-0242223P.  
PR 20-OCT-2000; 2000US-0242322P.  
PR 03-NOV-2000; 2000US-0245855P.  
PR 03-NOV-2000; 2000US-0245900P.  
PR 09-NOV-2000; 2000US-0247587P.  
PR 15-NOV-2000; 2000US-0249343P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Baughn MR, Graul RC, Walia NK, Gandhi AR, Hafalia AJA,  
XX Rankumar J, Tribouley CM, Thornton M, Kallick DA, Yao MG,  
XX Elliott VS, Burford N, Khan FA, Yue H, Lu Y, Arvizu C, Roopa R;

XX Human; gens; ds; G protein-coupled receptor; GPCR; nPCR; beGPCR;  
KW nG protein coupled receptor; communication; serpentine structure;  
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;  
KW genetic predisposition; brain; immune response; gene therapy;  
KW anxiety disorder; depression; bipolar disorder; schizophrenia;  
KW Huntington's disease; dyskinesia; manic depression; stroke;  
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;  
KW tranquiliser.  
XX Homo sapiens.  
OS WO200264789-A1.  
PN XX  
XX PD  
XX PP  
XX PR  
XX PA  
XX PI  
PI Lind P, Parodi LA, Vogeli G, Wood LS;  
DR WPI: 2002-674879/72.  
DR P-PSDB; ABQ93787.  
XX New nucleic acids and polypeptides of the nG protein-coupled receptor,  
PT useful for treating or diagnosing a mental disorder or a disorder  
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or  
PT Parkinson's disease.  
XX Example 1; Page 84-85; 244pp; English.  
XX The invention discloses an isolated human polypeptide, and encoding  
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the  
CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the  
CC communication between cells and their environment and are characterised  
CC by a serpentine structure that passes through the cell membrane seven  
CC times, hence the reason such receptors are sometimes called seven  
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are  
CC useful for identifying an nGPCR allelic variant that correlates with a  
CC mental disorder, for isolating an antibody that binds to an epitope of  
CC the polypeptide, for identifying a compound that binds the polypeptide or  
CC polynucleotide and/or modulates its biological activity, for screening a  
CC human subject to diagnose a disorder, or a genetic predisposition to a  
CC disorder, affecting the brain or a genetic disposition to the disorder,  
CC for identifying compounds useful for the treatment of a mental disorder  
CC and for identifying a compound useful as a modulator of binding between  
CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also  
CC useful for inducing an immune response in a mammal. The nucleic acid or  
CC polypeptide is particularly useful, using gene therapy, for treating e.g.  
CC anxiety disorders, depression, bipolar disorder, schizophrenia,  
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's  
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also  
CC be used for treating diabetes, inflammation or wounds. The sequences  
CC presented in ABS70202-ABS70248, ABS70338 and ABS70243 are the DNAs  
CC encoding the nGPCRs (also referred to as beGPCRs)  
XX Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 918; DB 6; Length 2525;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGCAGTCCCTATAGTGACACCACCACTTA 60  
DB |||||||GGGCGCAGCATACCTCCAGGAATTCCTCTTGCAGTCCCTATAGTGACACCACCACTTA 86  
QY 61 ATCAGCCTTACTTCACTAGTGTTATGGCGGGCTGGTGGGTGTCATTTCCTATCTTTTC 120  
DB 87 ATCAGCCTTACTTCACTAGTGTTATGGCGGGCTGGTGGGTGTCATTTCCTATCTTTTC 146



neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder; attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; ds.

*Homo sapiens.*

WO200136473-A2.

25-MAY-2001.

16-NOV-2000: 2000WO-US031581.

16-NOV-1999: 99US-0165838P.

17-NOV-1999; 99US-0166071F;  
19-NOV-1999; 99US-0166678P;

28-DEC-1999; 99US-01/3396P.  
22-FEB-2000: 2000US-0184129P.

28-FEB-2000; 2000US-018542IP.  
28-FEB-2000; 2000US-0185554P.

02-MAR-2000; 2000US-0186530P.  
03-MAR-2000: 2000US-0186811P.

09-MAR-2000; 2000US-0188114P.  
17-MAR-2000; 2000US-0190310P

21-MAR-2000; 2000US-0190800P.  
30-APR-2000; 2000US-0198568P.

02-MAY-2000; 2000US-0201190P.

25-MAY-2000; 2000US-0207094P.

(PHAA) PHARMACIA & UPJOHN CO

Vogeli G, Wood LS, Parodi L

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P-PSDB; AAG80969.

## New G protein-coupled receptors

100

100

(nGPCRx; where x is 1, 3, 4, 5

the coding sequence for one such G protein-coupled receptor. GPCRs are

transduction. The nG

preposition, a

ngPCR in a sample is useful as a diagnostic tool for diseases or

CNS disorders, infections such as HIV-1, metabolic and

nGPCRx activity have the utility for

disorders (e.g. schizophrenia, bipolar disorder, attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.

Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

Very Match 100.0%; Score 918; DB 4; Length 2525;

Best Local Similarity 100.0%, Freq: NO, Mismatches 0: Conservative 0: Mismatches 918: Conservative

1 ATGCCTGGCCACAAATACCTCCAGGAATTCCCTCTTGGATCCTATAGTGACACCCCACTTA 60

1 ATGCCTGGCCACAAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60

27	ATGCGCTGCCCAATACCTCCAGAAATTCCTCTTGGATCCCTATATAGTACACCCACCTTA	86
61	ATCAGCCCTCTACTTTCATAGTGTCTTATTTGCGGGCTGGTGGGTGTCAATTTCCATTTCTTTTC	120
87	ATCAGCCCTCTACTTTCATAGTGTCTTATTTGCGGGCTGGTGGGTGTCAATTTCCATTTCTTTTC	146
121	CTCCCTGGTGAATAATGAACACCCCGTCAGTAGTACACCAATGGCGGTCAATTAACCTTGGTGGT	180
147	CTCCTCGGTGAATAATGAACACCCCGTCAGTAGTACCAATGGCGGTCAATTAACCTTGGTGGT	206
181	GTCCACAGCGTTTTCTGTCTGACAGTGCCATTTTCGGTTCACTTACCTCATCAAGAAGACT	240
207	GTCCACAGCGTTTTCTGTCTGACAGTGCCATTTTCGGTTCACTTACCTCATCAAGAAGACT	266
241	TGGATGTTTTGGCTGCCCTCTCTGCAAAATTTGTGAGTGCCATGTGTCGACATCCACATGTAC	300
267	TGGATGTTTTGGCTGCCCTCTCTGCAAAATTTGTGAGTGCCATGTGTCGACATCCACATGTAC	326
301	CTCACGTTCTCTATTCTATGTGGTGATCCTGGTCAACAGATACCTCACTTCTTCAAGTGC	360
327	CTCACGTTCTCTATTCTATGTGGTGATCCTGGTCAACAGATACCTCACTTCTTCAAGTGC	386
361	TAAGACAAGTGGAAATCTTACAGAAATCTCATGTGCTGCGCAGTGCCTGGCATGTGG	420
387	TAAGACAAGTGGAAATCTTACAGAAATCTCATGTGCTGCGCAGTGCCTGGCATGTGG	446
421	ACGCTGGTGATGTCAATGTGGTACCCCTGGTTGTCTCCGGTATGGAATCATCATGAGAA	480
447	ACGCTGGTGATGTCAATGTGGTACCCCTGGTTGTCTCCGGTATGGAATCATCATGAGAA	506
481	TACAATGAGGAGCACTGTTTTAAATTTACAAAAGAGCTTGCTTTACACATATGTGAAAATC	540
507	TACAATGAGGAGCACTGTTTTAAATTTACAAAAGAGCTTGCTTTACACATATGTGAAAATC	566
541	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGCTGTGATTCGTGTGCTTCTCCAG	600
567	ATCAACTATATGATAGTCAATTTTGTCAATAGCCGTTGCTGTGATTCGTGTGCTTCTCCAG	626
601	GTCTTTCATCATTTAGTGTGATGGTGCAGAACTACGCCACTCTTTTACTATCCCAACAGGAG	660
627	GTCTTTCATCATTTAGTGTGATGGTGCAGAACTACGCCACTCTTTTACTATCCCAACAGGAG	686
661	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTCACTCCTGTTGTTTCTTCTCC	720
687	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTCACTCCTGTTGTTTCTTCTCC	746
721	TACCAAGTTCTTTTAGGATCTATTACTTCAATGTGTGACGCAATCCCAATGCCTGTAAACAGC	780
747	TACCAAGTTCTTTTAGGATCTATTACTTGAATGTGTGAGCCATTCCTAAATGCCTGTAAACAGC	806
781	AAGTTGTCAATTTTATACGAAATCTTCTTGAGTGTAAACAGCAATTAAGCTGTATGATTG	840
807	AAGTTGTCAATTTTATACGAAATCTTCTTGAGTGTAAACAGCAATTAAGCTGTATGATTG	866
841	CTTCTCTTTGCTTTTGGGGAGGCAATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900
867	CTTCTCTTTGCTTTTGGGGAGGCAATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	926
901	TGTGTTTTGTGCCGTTAG	918
927	TGTGTTTTGTGCCGTTAG	944

## RESULT 10

RESOLUTION  
ABS70242

ID ABS70242 standard; DNA; 2525 BP.

AC ABS70242:

DT 26-NOV-2002 (first entry)

XX DE DNA encoding human G protein-coupled receptor, nGPCR-16.

XX 19-NOV-2002 (first entry)  
DT Human GREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.  
XX  
DE  
XX GREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection;  
KW gene therapy; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200263004-A2.  
XX  
XX 15-AUG-2002.  
XX  
XX 06-FEB-2002; 2002WO-US003635.  
XX  
XX 07-FEB-2001; 2001US-0267322P.  
XX  
XX 23-FEB-2001; 2001US-0271215P.  
XX  
XX 08-MAR-2001; 2001US-0274551P.  
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XX 23-MAR-2001; 2001US-0278507P.  
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XX 30-MAR-2001; 2001US-0280597P.  
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XX 02-APR-2001; 2001US-0281107P.  
XX  
XX 06-APR-2001; 2001US-0282121P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Baughn ME, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
XX Kallick DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;  
XX Ramkumar J, Pei J, Tang YF, Yue H, Reddy R, Butford N, Lu DAM;  
XX Graul RC, Khan FA, Walsh RT, Ison CM, Richardson TW, Griffin JA;  
XX Warren BA, Yang J, Lee EA, Harland L;  
XX WPI; 2002-627557/67.  
XX  
XX P-PSDB; AAB71327.  
XX  
XX New human G-protein coupled receptors (GREC), useful for diagnosing or  
XX treating a disease or condition associated with decreased expression or  
XX over expression of functional GRECs e.g. cancer, Alzheimer's and  
XX Parkinson's.  
XX  
XX Claim 115; Page 213-214; 239pp; English.  
XX  
XX This invention describes novel polypeptides which have anti-HIV,  
XX antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
XX antibacterial, fungicide and protozoacide activity. The products of the  
XX invention are useful for treating a disease or condition associated with  
XX decreased expression or over expression of functional G-protein coupled  
XX receptors (GREC), while antibodies generated against the polypeptide of  
XX the invention are useful for diagnosing a condition or disease associated  
XX with the expression of GREC e.g. arteriosclerosis, cirrhosis, cancer,  
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
XX The compounds described in the invention can be used for gene therapy.  
XX AAF88580-AAR88627 encode the GREC proteins represented by AAB71322-  
XX AAB71369, described in the disclosure of the invention  
XX  
XX Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 918; DB 6; Length 1460;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 ATGCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 60  
DB 343 ATGCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTACACCCCACTTA 402  
XX  
XX 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTC 120  
XX

DB 403 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCCTTCCTTTTC 462  
QY 121 CTCCTGGTGAATTAACACCCCGTCACTCAGTCACCACTGCGGTCAATTAACCTTGGTGGT 180  
DB 463 CTCCTGGTGAATTAACACCCCGTCACTCAGTCACCACTGCGGTCAATTAACCTTGGTGGT 522  
QY 181 GTCCACAGCGTTTCTGCTGACAGTCCCAATTCGCTTGACCTACCTCATCAAGAGACT 240  
DB 523 GTCCACAGCGTTTCTGCTGACAGTCCCAATTCGCTTGACCTACCTCATCAAGAGACT 582  
QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCCATGCTGCACATCCCATGTAC 300  
DB 583 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCCATGCTGCACATCCCATGTAC 642  
QY 301 CTCACGTTCTTATATGTTGATACCTGGTGCACAGATACCTCATCTCTTCAAGTGC 360  
DB 643 CTCACGTTCTTATATGTTGATACCTGGTGCACAGATACCTCATCTCTTCAAGTGC 702  
QY 361 AAAGACAAAGTGGAAATTCACAGAAACTGCTGCTGGCTGCCAGTGGCATGTGG 420  
DB 703 AAAGACAAAGTGGAAATTCACAGAAACTGCTGCTGGCTGCCAGTGGCATGTGG 762  
QY 421 ACGTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCCATGAGAA 480  
DB 763 ACGTGGTGAATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCCATGAGAA 822  
QY 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGGAATTC 540  
DB 823 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGGAATTC 882  
QY 541 ATCAACTATATGATGATCAATTTTGTATAGCCCTGCTGTGATCTGTGGTCTTCCAG 600  
DB 883 ATCAACTATATGATGATCAATTTTGTATAGCCCTGCTGTGATCTGTGGTCTTCCAG 942  
QY 601 GTCTTCATCATATGTTGATGGTGCAGAGCTACGCCACTCTTTACTATCCACACAGAG 660  
DB 943 GTCTTCATCATATGTTGATGGTGCAGAGCTACGCCACTCTTTACTATCCACACAGAG 1002  
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTGTGTTTCTTCTCCC 720  
DB 1003 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTGTGTTTCTTCTCCC 1062  
QY 721 TACCAAGTCTTTAGATCTATTAAGTGTGACGATTCGAATCCCAATGCTGTAAACAGC 780  
DB 1063 TACCAGTCTTTTAGATCTATTAAGTGTGACGATTCGAATCCCAATGCTGTAAACAGC 1122  
QY 781 AAGGTTGCAATTTTAAACGAATCTTCTGAGTGTAAACGAATAGCTGCTATGATTG 840  
DB 1123 AAGGTTGCAATTTTAAACGAATCTTCTGAGTGTAAACGAATAGCTGCTATGATTG 1182  
QY 841 CTCTCTTTGCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATAATGCTTATGGAAT 900  
DB 1183 CTCTCTTTGCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATAATGCTTATGGAAT 1242  
QY 901 TGTGTTTGTGCGGTAG 918  
DB 1243 TGTGTTTGTGCGGTAG 1260  
XX  
XX RESULT 9  
XX AAB51009  
XX ID AAB51009 standard; DNA; 2525 BP.  
XX  
XX AC AAB51009;  
XX  
XX XX 28-AUG-2001 (first entry)  
XX  
XX XX Human nPCR16 coding sequence #2.  
XX  
XX XX G protein-coupled receptor; nPCR; seven transmembrane receptor;  
XX signal transduction; schizophrenia; thyroid disorder; renal failure;  
XX rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
XX cardiovascular disease; proliferative disorder; hormonal disorder;

DB 1119 TGTGTTTGTGCGGTAG 1136  
|||||  
RESULT 7  
AAAF8584  
ID AAP8584 standard; cDNA; 1340 BP.  
XX  
XX  
AC AAP8584;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
XX Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.  
XX  
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;  
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;  
KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;  
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;  
KW Parkinson's disease; Crohn's disease; constipation; infection;  
KW gene therapy; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200263004-A2.  
PN  
XX  
XX 15-AUG-2002.  
PD  
XX  
XX 06-FEB-2002; 2002WO-US003635.  
PF  
XX  
XX 07-FEB-2001; 2001US-0267322P.  
PR  
XX 23-FEB-2001; 2001US-0271215P.  
PR  
XX 08-MAR-2001; 2001US-0274551P.  
PR  
XX 23-MAR-2001; 2001US-0278507P.  
PR  
XX 02-APR-2001; 2001US-0280597P.  
PR  
XX 06-APR-2001; 2001US-0281107P.  
PR  
XX (INCY-) INCYTE GENOMICS INC.  
PA  
XX  
XX Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;  
PI Kallick DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;  
PI Ramkumar J, Pei J, Tang VT, Yue H, Reddy R, Butford N, Lu DM;  
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;  
PI Warren BA, Yang J, Lee EA, Harland L;  
XX  
XX WPI; 2002-627557/67.  
DR  
XX P-PSDB; AAB71326.  
DR  
XX  
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or  
PT treating a disease or condition associated with decreased expression or  
PT over expression of functional GCRs e.g. cancer, Alzheimer's and  
PT Parkinson's.  
XX  
XX Claim 114; Page 213; 239pp; English.  
PS  
XX  
XX This invention describes novel polypeptides which have anti-HIV,  
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,  
CC antibacterial, fungicide and protozoacide activity. The products of the  
CC invention are useful for treating a disease or condition associated with  
CC decreased expression or over expression of functional G-protein coupled  
CC receptors (GCREC), while antibodies generated against the polypeptide of  
CC the invention are useful for diagnosing a condition or disease associated  
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,  
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,  
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.  
CC The compounds described in the invention can be used for gene therapy.  
CC AAF8580-AAF8627 encode the GCREC proteins represented by AAB71322-  
XX AAB71369, described in the disclosure of the invention  
XX  
XX Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;  
XX

Query Match 100.0%; Score 918; DB 6; Length 1340;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTACACCCACTTA 60  
Db 223 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTACACCCACTTA 282  
Qy 61 ATCAGCCTCTACTTTCATAGTGTCTTATTTGGCGGCTGGTGGTGTCTATTTCTTTTC 120  
Db 283 ATCAGCCTCTACTTTCATAGTGTCTTATTTGGCGGCTGGTGGTGTCTATTTCTTTTC 342  
Qy 121 CTCTGTGTGAATGAACACCCCGTCACTGACACCACTGCGGTCAATTAATTTGGTGGTG 180  
Db 343 CTCTGTGTGAATGAACACCCCGTCACTGACACCACTGCGGTCAATTAATTTGGTGGTG 402  
Qy 181 GTCCACAGCCTTTTCTGTGACAGTGCATTTGCTTGCCTTACCTCATCAAGAAGACT 240  
Db 403 GTCCACAGCCTTTTCTGTGACAGTGCATTTGCTTGCCTCATCAAGAAGACT 462  
Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGTGCACATCCACATGTAC 300  
Db 463 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGTGCACATCCACATGTAC 522  
Qy 301 CTCACGTTCTTATTTCTATGTGTGATCCTGTCACAGATACCTCATCTTTCAAGTGC 360  
Db 523 CTCACGTTCTTATTTCTATGTGTGATCCTGTCACAGATACCTCATCTTTCAAGTGC 582  
Qy 361 AAAGACAAAGTGAATTTCTACAGAAATCTGATGTGTGTGCTGCCAGTGTGCATGTGG 420  
Db 583 AAAGACAAAGTGAATTTCTACAGAAATCTGATGTGTGTGCTGCCAGTGTGCATGTGG 642  
Qy 421 ACGCTGGTATTTCTGATGTGTGATACCTGTTGTTCTCCGGTATGGAATCCATGAGGAA 480  
Db 643 ACGCTGGTATTTCTGATGTGTGATACCTGTTGTTCTCCGGTATGGAATCCATGAGGAA 702  
Qy 481 TACAATGAGGAGCACTGTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540  
Db 703 TACAATGAGGAGCACTGTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 762  
Qy 541 ATCAACTATATAGTATGATCAATTTTGTCAAGCCGTTGTGTGATTTCTGTTCTTCCAG 600  
Db 763 ATCAACTATATAGTATGATCAATTTTGTCAAGCCGTTGTGTGATTTCTGTTCTTCCAG 822  
Qy 601 GTCTTCATCATTTATGTTGATGTGAGAGTACGCCACTCTTTTACTATCCACACAGGAG 660  
Db 823 GTCTTCATCATTTATGTTGATGTGAGAGTACGCCACTCTTTTACTATCCACACAGGAG 882  
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTCTTGTGTTCTTCTCC 720  
Db 883 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTCTTGTGTTCTTCTCC 942  
Qy 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAACAGC 780  
Db 943 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAACAGC 1002  
Qy 781 AAGTTGCAATTTTATACGAAATCTTTTGTGAGTGTAAACAGCAATTAGTCTATGTTG 840  
Db 1003 AAGTTGCAATTTTATACGAAATCTTTTGTGAGTGTAAACAGCAATTAGTCTATGTTG 1062  
Qy 841 CTCTCTTTTCTTTGGGGAAGCCATTGTTTAAACAAAGATATTTGCTTTATGGAAT 900  
Db 1063 CTCTCTTTTCTTTGGGGAAGCCATTGTTTAAACAAAGATATTTGCTTTATGGAAT 1122  
Qy 901 TGTGTTTGTGCGGTAG 918  
Db 1123 TGTGTTTGTGCGGTAG 1140  
RESULT 8  
AAAF8585  
ID AAP8585 standard; cDNA; 1460 BP.  
XX  
AC AAF8585;

QY	781	AGGTTGCATTTTATTAACGGAATCTTCTTGAGTGTAAACGCAATTAAGCTGCTATGATTGG	840
Db	781	AGGTTGCATTTTATTAACGGAATCTTCTTGAGTGTAAACGCAATTAAGCTGCTATGATTGG	840
QY	841	CTTCTCTTTGCTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATCGAAT	900
Db	841	CTTCTCTTTGCTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATCGAAT	900
QY	901	TGTGTTTTGTGCCGTTAG	918
Db	901	TGTGTTTTGTGCCGTTAG	918

Query Match	100.0%;	Score 918;	DB 6;	Length 1336;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 918;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA	60	
DB	219	ATGCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA	278	
QY	61	ATCAGCCTCTACCTTCATAGTGCTTATTTGGCGGCTGGTGGGTGCTATTTCCATCTCTTTTC	120	
DB	279	ATCAGCCTCTACCTTCATAGTGCTTATTTGGCGGCTGGTGGGTGCTATTTCCATCTCTTTTC	338	
QY	121	CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGCGGTGCATTAACCTTGGTGGTG	180	
DB	339	CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGCGGTGCATTAACCTTGGTGGTG	398	
QY	181	GTCACAGCGGTTTTCTGTGACAGTGCCCATTTGCTTTGACCTCATCAAGAAGACT	240	
DB	399	GTCACAGCGGTTTTCTGTGACAGTGCCCATTTGCTTTGACCTCATCAAGAAGACT	458	
QY	241	TGATGTTGGGCTGCGCTTCGCAAAATTTGTAGTGCCATGTCGACATCCACATGTAC	300	
DB	459	TGATGTTGGGCTGCGCTTCGCAAAATTTGTAGTGCCATGTCGACATCCACATGTAC	518	
QY	301	CTCACGTTCTATTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC	360	
DB	519	CTCACGTTCTATTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC	578	
QY	361	AAAGACAAAGTGAATTTACAGAAAACCTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG	420	
DB	579	AAAGACAAAGTGAATTTACAGAAAACCTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG	638	
QY	421	ACGCTGGTGATCTCATTTGTGTGATGACCTCGTGGTGTCTCCGGTATGGAATCCATGAGAA	480	
DB	639	ACGCTGGTGATCTCATTTGTGTGATGACCTCGTGGTGTCTCCGGTATGGAATCCATGAGAA	698	
QY	481	TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC	540	
DB	699	TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC	758	
QY	541	ATCAACTATATGATAGTCATTTTGTTCATAGCCGTTGCTGTGATTCGTGTGCTTCCAG	600	
DB	759	ATCAACTATATGATAGTCATTTTGTTCATAGCCGTTGCTGTGATTCGTGTGCTTCCAG	818	
QY	601	GTCTTCATCATTTATGTTGATGGTGAGAGCTACGGCACTCTTTTACTATCCCAACAGGAG	660	
DB	819	GTCTTCATCATTTATGTTGATGGTGAGAGCTACGGCACTCTTTTACTATCCCAACAGGAG	878	
QY	661	TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGTGATCCTGTGTTGTTTCCCTCCC	720	
DB	879	TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGTGATCCTGTGTTGTTTCCCTCCC	938	
QY	721	TACAGTCTCTTAGGATCTATTACTTTGAATGTTGTGACGCATTCCAATGCTGTAAACAGC	780	
DB	939	TACAGTCTCTTAGGATCTATTACTTTGAATGTTGTGACGCATTCCAATGCTGTAAACAGC	998	
QY	781	AAGTTGCAATTTTATAACGAAATCTTCTTGTAGTGTTAACAGCAATTAGTGTCTATGATTG	840	
DB	999	AAGTTGCAATTTTATAACGAAATCTTCTTGTAGTGTTAACAGCAATTAGTGTCTATGATTG	1058	
QY	841	CTTCTCTTTGTCTTTGGGGAGGCCATCGTTTAAAGCAAAAGATAATTGGCTTATGGAAT	900	
DB	1059	CTTCTCTTTGTCTTTGGGGAGGCCATCGTTTAAAGCAAAAGATAATTGGCTTATGGAAT	1118	
QY	901	TGTGTTTTGTGCGGTTAG	918	

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTGTTGTTCTTCCC 720  
 Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTGTTGTTCTTCCC 720  
 QY 721 TACCAAGTTCCTTAGCATCTATTAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840  
 Db 721 TACCAAGTTCCTTAGCATCTATTAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840  
 QY 781 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840  
 Db 781 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840  
 QY 841 CTTCTCTTTGCTTTGGGGAGGCAATGCTTGAATGTTGAGCGCAATCCAAATGCGCTGAACAGC 900  
 Db 841 CTTCTCTTTGCTTTGGGGAGGCAATGCTTGAATGTTGAGCGCAATCCAAATGCGCTGAACAGC 900  
 QY 901 TGTGTTTGTGCGGTAG 918  
 Db 901 TGTGTTTGTGCGGTAG 918

RESULT 5  
 AAL57070  
 ID AAL57070 standard; DNA; 1040 BP.  
 AC AAL57070;  
 DT 17-SEP-2003 (first entry)  
 DE Human G-protein coupled receptor GAVE18 DNA sequence.  
 KW Human G-protein coupled receptor; GAVE18; signal transduction;  
 KW inflammation; physiological immunological response; anti-inflammatory;  
 KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;  
 KW chromosomal mapping; tissue typing; forensic biology;  
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;  
 KW rheumatoid arthritis; gene; ds.  
 OS Homo sapiens.

Key Location/Qualifiers  
 CDS 1..918  
 FT /\*tag= a  
 FT /product= "GAVE18 protein"  
 WO2003042399-A2.  
 22-MAY-2003.  
 08-NOV-2002; 2002WO-US035887.  
 13-NOV-2001; 2001US-0354150P.  
 22-MAR-2002; 2002GB-00006891.  
 (AVET ) AVENTIS PHARM INC.  
 Eisingdrelo H, Cai J, Busch SJ, Gassenhuber J;  
 WPI; 2003-457496/43.  
 P-PSDB; RAO27265.  
 New GAVE18 polypeptide and nucleic acid molecule encoding the  
 polypeptide, useful for preventing and treating a disease or disorder  
 associated with aberrant expression or activity of GAVE18, e.g. asthma or  
 rheumatoid arthritis.  
 Claim 1; Fig 5; 88pp; English.  
 This invention relates to a novel G-protein coupled receptor (GAVE18)  
 that is involved in signal transduction in respect to inflammation and  
 the physiological immunological response. Molecules which may modulate  
 the signalling activity or signal transduction of the receptor may be

CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The  
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for  
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18  
 CC proteins and antibodies may be useful in screening assays, detection  
 CC assays (for example chromosomal mapping, tissue typing or forensic  
 CC biology), or predictive medicine (for example diagnostic assays;  
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The  
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse  
 CC agonist and antagonist are also useful for preventing and treating a  
 CC disease or disorder associated with aberrant expression or activity of  
 CC GAVE18, such as inflammation and immunological-related diseases or  
 CC disorders, for example asthma, chronic obstructive pulmonary disease or  
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding  
 CC the GAVE18 protein of the invention  
 XX  
 SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 8; Length 1040;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTTATAGTGACACCCCACTTA 60  
 Db 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTTATAGTGACACCCCACTTA 60  
 QY 61 ATCAGCCTCTACTTCTATAGTCTTATGCGGGCTGCTGGGTGTCATTTCCATTCCTTTC 120  
 Db 61 ATCAGCCTCTACTTCTATAGTCTTATGCGGGCTGCTGGGTGTCATTTCCATTCCTTTC 120  
 QY 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATCGCGGTCAATTAACCTGTGGTG 180  
 Db 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATCGCGGTCAATTAACCTGTGGTG 180  
 QY 181 GTCCACAGGTTTTCTGCTGACAGGCCATTTGCGCTGACCTACTCTCAAGAGACT 240  
 Db 181 GTCCACAGGTTTTCTGCTGACAGGCCATTTGCGCTGACCTACTCTCAAGAGACT 240  
 QY 241 TGGATGTTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
 Db 241 TGGATGTTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
 QY 301 CTCACGTTCTTATCTATGTTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360  
 Db 301 CTCACGTTCTTATCTATGTTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360  
 QY 361 AAAGACAAAGTGGAAATCTACAGAAATCTGCTGCTGCCAGTCTGCCATGTGG 420  
 Db 361 AAAGACAAAGTGGAAATCTACAGAAATCTGCTGCTGCCAGTCTGCCATGTGG 420  
 QY 421 AGCTGGTGATGTCATTTGTCACCCCTGTTGTCCTCCGGTATGGAATCCATGAGGAA 480  
 Db 421 AGCTGGTGATGTCATTTGTCACCCCTGTTGTCCTCCGGTATGGAATCCATGAGGAA 480  
 QY 481 TACAATGAGGAGCCTGTTTTAAATTTCAAGAGCTTGTTCACACATATCTGAAAATC 540  
 Db 481 TACAATGAGGAGCCTGTTTTAAATTTCAAGAGCTTGTTCACACATATCTGAAAATC 540  
 QY 541 ATCAACTATATGATGTCATTTTGTATAGCGTTGCTGTGATTTCTGTGTCTTCCAG 600  
 Db 541 ATCAACTATATGATGTCATTTTGTATAGCGTTGCTGTGATTTCTGTGTCTTCCAG 600  
 QY 601 GTCTTCATCATTTGTTGATGTCGAGAGCTACCGCACTCTTTACTATCCACAGGAG 660  
 Db 601 GTCTTCATCATTTGTTGATGTCGAGAGCTACCGCACTCTTTACTATCCACAGGAG 660  
 QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTGTTGTTCTTCCC 720  
 Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTGTTGTTCTTCCC 720  
 QY 721 TACCAGTCTCTTAGGATCTTACTTGAATGTTGAGCGCAATCCAAATGCGCTGAACAGC 780  
 Db 721 TACCAGTCTCTTAGGATCTTACTTGAATGTTGAGCGCAATCCAAATGCGCTGAACAGC 780

DB 361 AAAGCAAAAGTGAATCTACAGAAAATGCGATGCTGGTCCAGTGGCATGTGG 420  
QY 421 AGCTGGTGAATGTCATGTTGTACCCCTGGTGTCTCCGGTATGGAATCATGAGAA 480  
DB 421 AGCTGGTGAATGTCATGTTGTACCCCTGGTGTCTCCGGTATGGAATCATGAGAA 480  
QY 481 TACAATGAGGAGCACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540  
DB 481 TACAATGAGGAGCACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540  
QY 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTCTTTGCTTCCAG 600  
DB 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTCTTTGCTTCCAG 600  
QY 601 GTCCTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660  
DB 601 GTCCTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660  
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCTTTGTTGTTCTTCCC 720  
DB 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCTTTGTTGTTCTTCCC 720  
QY 721 TACCAAGTCTTATGATCTATTTACTTGAATGTTGAGCAGCATCCCAATGCTTAAACAGC 780  
DB 721 TACCAAGTCTTATGATCTATTTACTTGAATGTTGAGCAGCATCCCAATGCTTAAACAGC 780  
QY 781 AAGGTGTCATTTATAACGAATCTTCTTGAAGTGAACAGCAATTAGCTGTATGATTG 840  
DB 781 AAGGTGTCATTTATAACGAATCTTCTTGAAGTGAACAGCAATTAGCTGTATGATTG 840  
QY 841 CTTCTCTTTGCTTTGGGGGAGCCATTTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900  
DB 841 CTTCTCTTTGCTTTGGGGGAGCCATTTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900  
QY 901 TGTGTTTGTGCGGTTAG 918  
DB 901 TGTGTTTGTGCGGTTAG 918

## RESULT 4

ABZ59171  
ID ABZ59171 standard; DNA; 918 BP.  
AC ABZ59171;  
XX  
XX 28-APR-2003 (first entry)  
XX Human TGR343 protein encoding DNA.  
XX  
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;  
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;  
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;  
KW immunosuppressive; antiinflammatory; gene; da.

Homo sapiens.

Key Location/Qualifiers  
CDS 1..918  
FT /\*tag= a  
FT /product= "TGR343"

W02003004678-A2.

16-JAN-2003.

01-JUL-2002; 2002NO-US020860.

03-JUL-2001; 2001US-0302800P.

(TULA-) TULARIX INC.

Tian H, Dai K, Chen J, Zhao J, Cutler G;

DR WPI: 2003-210368/20.  
XX P-PSDB; ABP71378.  
FT New G-protein coupled receptor polypeptides designated TGR2, TGR38,  
TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs  
for treating or preventing e.g. asthma, multiple sclerosis, stroke or  
nephrolithiasis.

XX Claim 7; Page 61; 74pp; English.

XX The invention provides new G-protein coupled receptor (GPCR) polypeptides  
designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding  
polynucleotides. The polypeptides can be expressed by standard DNA  
recombination methodology. The polypeptides are useful for screening or  
identifying modulators of GPCR or signal transduction. The modulators of  
signal transduction are useful for treating or preventing TGR-associated  
disorders, e.g. asthma, multiple sclerosis or kidney disease. The  
polypeptides are useful as targets for diagnosing or treating e.g.  
epilepsy, stroke, neurodegeneration, hypernatremia, hyperprolactinemia,  
asymptomatic urinary abnormalities, hypertension, nephrolithiasis,  
cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute  
inflammatory dermatoses. The present sequence represents a human TGR343  
protein encoding DNA

XX Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 7; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60

DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTATGCTAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATCTTTTC 120

DB 61 ATCAGCCTCTACTTATGCTAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATCTTTTC 120

QY 121 CTCCTGGTGAATGAACACCCGTCAGTGACACCAATGCGGTCATTAACCTTGTGTG 180

DB 121 CTCCTGGTGAATGAACACCCGTCAGTGACACCAATGCGGTCATTAACCTTGTGTG 180

QY 181 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTTCGTTGACCTCATCAAGAGACT 240

DB 181 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTTCGTTGACCTCATCAAGAGACT 240

QY 241 TGGATGTTGGGTGCCCTTCGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300

DB 241 TGGATGTTGGGTGCCCTTCGCAAAATTTGTAGTGCCATGCTGCACATCCCATGTAC 300

QY 301 CTCAGTTCTTATTTCTATGTTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360

DB 301 CTCAGTTCTTATTTCTATGTTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360

QY 361 AAAGCAAAAGTGAATTTCTACAGAAAATCGATGCTGTGGCTGCCAGTGTGGCATGTGG 420

DB 361 AAAGCAAAAGTGAATTTCTACAGAAAATCGATGCTGTGGCTGCCAGTGTGGCATGTGG 420

QY 421 AGCTGGTGAATGTCATTTGTCACCCCTGGTGTCTCCGGTATGGAATCCCATGAGAA 480

DB 421 AGCTGGTGAATGTCATTTGTCACCCCTGGTGTCTCCGGTATGGAATCCCATGAGAA 480

QY 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCCTTACATATGTGAAATC 540

DB 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCCTTACATATGTGAAATC 540

QY 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTCTTGTGGTCTTCCAG 600

DB 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATCTCTTGTGGTCTTCCAG 600

QY 601 GTCCTTCATCATTTATGTTGATGTTGTCAGAGCTACGCCACTCTTTACTATCCACAGGAG 660

DB 601 GTCCTTCATCATTTATGTTGATGTTGTCAGAGCTACGCCACTCTTTACTATCCACAGGAG 660

Db 1 ATGCTGGCCCAATATACCTCCAGGAATTCCTTTGGCATCCTATAGTGACACACCCCACTTA 60  
 Qy 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGCATTTCCATTCCTTTTC 120  
 Db 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGCATTTCCATTCCTTTTC 120  
 Qy 121 CTCCTGGTGAATAATGAACACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTTGGTGGT 180  
 Db 121 CTCCTGGTGAATAATGAACACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTTGGTGGT 180  
 Qy 181 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCACTCAAGAACT 240  
 Db 181 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCACTCAAGAACT 240  
 Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATCTGACATCCATCCACATGTAC 300  
 Db 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATCTGACATCCATCCACATGTAC 300  
 Qy 301 CTCAGCTTCCTATTCATAGTGGTATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360  
 Db 301 CTCAGCTTCCTATTCATAGTGGTATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360  
 Qy 361 AAGACAAAGTGAATCTCAGAAAACCTGCATGCTGGTGGCTGCAGTGCCTGGCATGTGG 420  
 Db 361 AAGACAAAGTGAATCTCAGAAAACCTGCATGCTGGTGGCTGCAGTGCCTGGCATGTGG 420  
 Qy 421 ACGTGGTATGTCAATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480  
 Db 421 ACGTGGTATGTCAATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480  
 Qy 481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTAATC 540  
 Db 481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTGTACACATATGTAATC 540  
 Qy 541 ATCAACTATATGATGATCATTTTGTATAGCCGTGCTGTGATTCCTTGGTCTTCAG 600  
 Db 541 ATCAACTATATGATGATCATTTTGTATAGCCGTGCTGTGATTCCTTGGTCTTCAG 600  
 Qy 601 GTCTTCATATGTTGATGGTGCAGAGCTAGCCACTTTTACTATCCACAGAG 660  
 Db 601 GTCTTCATATGTTGATGGTGCAGAGCTAGCCACTTTTACTATCCACAGAG 660  
 Qy 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720  
 Db 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720  
 Qy 721 TACAGTCTTTAGATCTATCTTGAATGTTGTGACGATTCATCCATGCTGTAAAGC 780  
 Db 721 TACAGTCTTTAGATCTATCTTGAATGTTGTGACGATTCATCCATGCTGTAAAGC 780  
 Qy 781 AAGTTGCTATTTTAAACGAAATCTTCTTGATGTGAACAGCAATAGCTGTATGATTG 840  
 Db 781 AAGTTGCTATTTTAAACGAAATCTTCTTGATGTGAACAGCAATAGCTGTATGATTG 840  
 Qy 841 CTTCCTTTTGTCTTTGGGGAAGCAATGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900  
 Db 841 CTTCCTTTTGTCTTTGGGGAAGCAATGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900  
 Qy 901 TGTGTTTGTCCCGTTAG 918  
 Db 901 TGTGTTTGTCCCGTTAG 918

## RESULT 3

ABT04867

ID ABT04867 standard; cDNA; 918 BP.

XX

AC ABT04867;

XX

DT 11-OCT-2002 (first entry)

XX

DE Human G protein coupled receptor hrUP29 coding sequence.

XX

KW Human; G-protein coupled receptor; GPCR; hrUP28; hrUP30; hrUP31;  
 KW hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37; gene; ss.  
 OS Homo sapiens.  
 PN WO200242461-A2.  
 PD 30-MAY-2002.  
 XX 26-NOV-2001; 2001WO-US044386.  
 XX 27-NOV-2000; 2000US-0253404P.  
 PR 12-DEC-2000; 2000US-0255366P.  
 PR 20-FEB-2001; 2001US-0270266P.  
 PR 20-FEB-2001; 2001US-0270286P.  
 PR 06-APR-2001; 2001US-0282032P.  
 PR 06-APR-2001; 2001US-0282356P.  
 PR 06-APR-2001; 2001US-0282358P.  
 PR 06-APR-2001; 2001US-0282365P.  
 PR 14-MAY-2001; 2001US-0290917P.  
 PR 31-JUL-2001; 2001US-0309208P.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;  
 XX  
 DR WPI; 2002-566565/60.  
 DR P-PSDB; ABJ04069.  
 XX  
 PT Novel endogenous and non-endogenous versions of G protein-coupled  
 PT receptor useful for identification of candidate compounds as receptor  
 PT agonists or antagonists for use as therapeutic agents.  
 XX  
 PS Claim 7; Page 56-57; 84pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC several human G-protein coupled receptors (GPCRs). These can be used in  
 CC the identification of candidate compounds as receptor agonists or inverse  
 CC agonists having applicability as therapeutic agents. The present sequence  
 CC is a GPCR coding sequence of the invention  
 XX  
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCCAATATACCTCCAGGAATTCCTTTGGCATCCTATAGTGACACCCCACTTA 60  
 Db 1 ATGCTGGCCCAATATACCTCCAGGAATTCCTTTGGCATCCTATAGTGACACCCCACTTA 60  
 Qy 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGCATTTCCATTCCTTTTC 120  
 Db 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGGTGGTGGTGCATTTCCATTCCTTTTC 120  
 Qy 121 CTCCTGGTGAATAATGAACACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTTGGTGGT 180  
 Db 121 CTCCTGGTGAATAATGAACACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTTGGTGGT 180  
 Qy 181 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCACTCAAGAACT 240  
 Db 181 GTCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCACTCAAGAACT 240  
 Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATCTGACATCCATCCACATGTAC 300  
 Db 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATCTGACATCCATCCACATGTAC 300  
 Qy 301 CTCAGCTTCCTATTCATAGTGGTATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360  
 Db 301 CTCAGCTTCCTATTCATAGTGGTATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360  
 Qy 361 AAGACAAAGTGAATCTCAGAAAACCTGCATGCTGGTGGCTGCAGTGCCTGGCATGTGG 420

CC The present invention provides the protein and coding sequences of a  
CC novel human testis-originated G protein-coupled receptor protein TGR10.  
CC The sequences can be used in the development of drugs for the treatment  
CC of diseases of the central nervous system, inflammations, diseases of the  
CC circulatory system, cancer, metabolic diseases, immunological diseases  
CC and diseases of the gastrointestinal system. The present sequence is the  
CC coding sequence of the invention  
XX  
SQ

Query Match 100.0%; Score 918; DB 6; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCACAAATACCTCCAGGAATCTCTTGATGATCTATAGTGACACCCACCTTA 60  
Db 1 ATGCTGGCCACAAATACCTCCAGGAATCTCTTGATGATCTATAGTGACACCCACCTTA 60  
Qy 61 ATCAGCCTTACTTCTAGTGTATTGCGGGCTGGTGGTGTATTTCCATTCTTTTC 120  
Db 61 ATCAGCCTTACTTCTAGTGTATTGCGGGCTGGTGGTGTATTTCCATTCTTTTC 120  
Qy 121 CTCCTGGTGAATAAGAACCCGGTCAGTGACACCAATCGCGGTCAATTAACCTTGTTGGT 180  
Db 121 CTCCTGGTGAATAAGAACCCGGTCAGTGACACCAATCGCGGTCAATTAACCTTGTTGGT 180  
Qy 181 GTCCACAGGTTTCTTCTGTCAGAGGCCATTTGCTTGCCTTACCTACTCATCAAGAGACT 240  
Db 181 GTCCACAGGTTTCTTCTGTCAGAGGCCATTTGCTTGCCTTACCTACTCATCAAGAGACT 240  
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
Db 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300  
Qy 301 CTCACGTTCTATCTATGTGTGATCTGTCACCAAGATCTCTTCTTCAAGTGC 360  
Db 301 CTCACGTTCTATCTATGTGTGATCTGTCACCAAGATCTCTTCTTCAAGTGC 360  
Qy 361 AAAGACAAAGTGAATCTTACGAAATCTGCAAAATTTGAGTGCCATGCTGCACATGTCG 420  
Db 361 AAAGACAAAGTGAATCTTACGAAATCTGCAAAATTTGAGTGCCATGCTGCACATGTCG 420  
Qy 421 AGCTGGTGAATGATCTATGTTGTTGACCCCTGTTGTCCTCCGGTATGGAATCCATGAGAA 480  
Db 421 AGCTGGTGAATGATCTATGTTGTTGACCCCTGTTGTCCTCCGGTATGGAATCCATGAGAA 480  
Qy 481 TACAATGAGGACGACCTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540  
Db 481 TACAATGAGGACGACCTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540  
Qy 541 ATCAACTATATGATGATCTATTTTGTATAGCCGTTGCTGTGATCTGTGTTCTTCCAG 600  
Db 541 ATCAACTATATGATGATCTATTTTGTATAGCCGTTGCTGTGATCTGTGTTCTTCCAG 600  
Qy 601 GTCTTCATATATGTTGATGGTGACAGAGCTACGCCACTCTTACTATCCACAGGAG 660  
Db 601 GTCTTCATATATGTTGATGGTGACAGAGCTACGCCACTCTTACTATCCACAGGAG 660  
Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCCTGTTTCTTCTTCC 720  
Db 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCCTGTTTCTTCTTCC 720  
Qy 721 TACAGTCTTTAGGATCTATTTGATGTTGTCAGCATTCACATCCATCCCTGTACACG 780  
Db 721 TACAGTCTTTAGGATCTATTTGATGTTGTCAGCATTCACATCCATCCCTGTACACG 780  
Qy 781 AAGGTTGCAATTTTATACGAAATCTTCTTGTAGTGTAAACAGCAATTAGCTGCTATGTTG 840  
Db 781 AAGGTTGCAATTTTATACGAAATCTTCTTGTAGTGTAAACAGCAATTAGCTGCTATGTTG 840  
Qy 841 CTTCTCTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAGATTAATGGCTTATGGAAT 900  
Db 841 CTTCTCTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAGATTAATGGCTTATGGAAT 900

Qy 901 TGTGTTTGTGCGGTAG 918  
Db 901 TGTGTTTGTGCGGTAG 918  
RESULT 2  
ABA00160  
ID ABA00160 standard; cDNA; 918 BP.  
XX  
AC ABA00160;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE PFI-021 cDNA.  
XX  
KW Gene; human; G-protein coupled receptor; GPCR; PFI-021;  
KW peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;  
KW respiratory; neurology; psychology; urogenital disease;  
KW reproductive dysfunction; sexual dysfunction; cancer; tissue repair;  
KW dermatology; skin pigmentation; photoaging; frailty; osteoporosis;  
KW metabolic disease; cardiovascular disease; sleep disorder; hair loss;  
KW gastrointestinal disease; anti-infection; sensory organ disorder; ss.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FT 1..918  
CDS /\*tag= a  
FT /\*product= "PFI-021"  
XX  
EP1225183-A2.  
XX  
PD 24-JUL-2002.  
XX  
PF 09-JAN-2002; 2002EP-00250128.  
XX  
PR 23-JAN-2001; 2001GB-00001739.  
XX  
PA (PFI-021) PFIZER LTD.  
PA (PFI-021) PFIZER INC.  
XX  
PI Harland L;  
XX  
DR WPI; 2002-601226/65.  
DR P-PSDB; AAG79446.  
XX  
PT New human G-protein coupled receptor involved in signal transduction,  
PT useful to treat disorders associated with its expression or activity such  
PT as inflammation, allergy and cancer.  
XX  
PS Claim 1; Fig 1; 8pp; English.  
XX  
CC This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.  
CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA  
CC libraries from peripheral blood mononuclear cells. Two ESTs have been  
CC identified in libraries derived from breast mRNA. PFI-021 and the  
CC corresponding cDNA are used to treat a patient needing altered activation  
CC or expression of a GPCR, such as inflammation, allergy and respiratory,  
CC neurology, psychology, urogenital disease, reproductive and sexual  
CC dysfunction/disorders, cancer, tissue repair, dermatology, skin  
CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic  
CC disease, cardiovascular disease, gastro-intestinal disease, anti-  
CC infection, sensory organ disorders, sleep disorders and hair loss  
XX  
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;  
Query Match 100.0%; Score 918; DB 6; Length 918;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATCTCTTGATGATCTATAGTGACACCCACCTTA 60



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:49:39 ; Search time 452 Seconds  
(without alignments)  
8627.978 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgctggccacaatacctc.....attgtgtttgtgcgcttag 918

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 12

Total number of hits satisfying chosen parameters: 258324

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: geneseq1990s.\*
- 3: geneseq2000s.\*
- 4: geneseq2001as.\*
- 5: geneseq2001bs.\*
- 6: geneseq2002s.\*
- 7: geneseq2003as.\*
- 8: geneseq2003bs.\*
- 9: geneseq2003cs.\*
- 10: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6	AAL44713 Human tes
2	918	100.0	918	6	ABA00160 PPT-021 c
3	918	100.0	918	6	ABT04867 Human G p
4	918	100.0	918	7	ABZ59171 Human TGR
5	918	100.0	1040	8	AAL57070 Human G-P
6	918	100.0	1336	6	AAT88583 Human GCR
7	918	100.0	1340	6	AAT88584 Human GCR
8	918	100.0	1460	6	AAT88585 Human GCR
9	918	100.0	2525	4	AAL51009 Human nGP
10	918	100.0	2525	6	ABS70242 DNA encod
11	918	100.0	113306	9	ADC86554 Human GPC
12	887	96.6	1499	6	ADC86554 Human GPC
13	867	94.4	1051	6	ABK87351 Human G-P
14	867	94.4	1684	6	AAL53413 Human CDN
15	864	94.1	939	6	AAL53414 939 nt co
16	690	75.2	972	9	ADC12789 Human GPC
17	306	33.3	447	4	AAL50979 Human nGP
18	306	33.3	447	6	ABS70212 DNA encod
19	162	17.6	479	4	AAK56763 Human imm
20	39	4.2	29	6	ABK87363 Human G p
21	29	3.2	29	6	ABT04881 Human G p
22	28	3.1	28	6	ABT04880 Human G p
23	27	2.9	810	9	ADB78584 Mouse G-p

24	26	2.8	26	6	AAL44718	Testis or
25	26	2.8	26	6	ABT04906	Human G p
C 26	25	2.7	25	8	AAL57075	TaqMan pr
C 27	24	2.6	24	4	AAH51055	Oligonuc
C 28	24	2.6	24	4	AAH51084	Human nGP
C 29	24	2.6	24	6	AAL44715	Testis or
C 30	24	2.6	24	6	ABS70288	nGPCR-x r
C 31	24	2.6	24	6	ABS70317	PCR prime
C 32	24	2.6	24	8	AAL57073	TaqMan pr
C 33	24	2.6	26	6	ABT04878	Human G p
C 34	24	2.6	52	4	AAH51085	Human nGP
C 35	24	2.6	52	4	AAH51056	Oligonuc
C 36	24	2.6	52	6	ABS70318	PCR prime
C 37	24	2.6	52	6	ABS70289	nGPCR-x r
C 38	23	2.5	23	4	AAH51057	Oligonuc
C 39	23	2.5	23	4	AAH51086	Human nGP
C 40	23	2.5	23	6	ABS70319	PCR prime
C 41	23	2.5	23	6	ABS70290	nGPCR-x r
C 42	23	2.5	23	7	ABZ59182	Human TGR
C 43	23	2.5	31	6	ABT04879	Human G p
C 44	23	2.5	31	6	ABT04907	Human G p
C 45	23	2.5	34	4	AAH51033	Human nGP

#### ALIGNMENTS

RESULT 1					
AAL44713					
ID	AAL44713 standard; DNA; 918 BP.				
XX					
AC	AAL44713;				
XX					
DT	03-MAY-2002 (first entry)				
XX					
DE	Human testis originated G-protein coupled receptor TGR10 coding sequence.				
XX					
KW	Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;				
KW	cytostatic; immunomodulator; cardiact; neuroprotective; gene therapy;				
KW	inflammation; nervous system disease; circulatory system disease; cancer;				
KW	metabolic disease; immunological disease; gastrointestinal disease; gene;				
XX	ds.				
XX	Homo sapiens.				
XX					
PH	Key Location/Qualifiers				
FT	1..918				
FT	/*tag= a				
FT	/product= "TGR10"				
XX					
XX	WO200196567-A1.				
XX					
PD	20-DEC-2001.				
XX					
PP	14-JUN-2001; 2001WO-JP005061.				
XX					
PR	15-JUN-2000; 2000JP-00184596.				
XX					
PR	19-JUL-2000; 2000JP-00223887.				
XX					
PA	(TAKE ) TAKEDA CHEM IND LTD.				
XX					
PI	Moriya T, Ito T, Shintani Y, Miyajima N;				
XX					
DR	WPI; 2002-098071/13.				
XX					
DR	P-PSDB; AAM48989.				
XX					
PT	Human testis-originated G protein-coupled receptor protein TGR10 and				
PT	encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.				
PT	diseases of central nervous system, inflammations and diseases of				
PT	circulatory system.				
XX					
PS	Claim 5; Page 99; 110pp; Japanese.				
XX					

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Query Match      1.9%; Score 17; DB 4; Length 801;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGTGTTTAAATTCACAA 512
DB 18 TGTGTTTAAATTCACAA 2

RESULT 14
US-09-489-039A-1185/c
; Sequence 1185, Application US/09489039A
; Patent No. 6810836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1185
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1185

Query Match      1.9%; Score 17; DB 4; Length 978;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 ACCACCATGGGGTTCAT 167
DB 260 ACCACCATGGGGTTCAT 244

RESULT 15
US-09-833-381-461
; Sequence 461, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 461
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-461

Query Match      1.9%; Score 17; DB 4; Length 1057;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 GTTGATGGTGCAGAGC 631
DB 704 GTTGATGGTGCAGAGC 720

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Db 3981 TATTGGCGGCTGCTGGG 3998

RESULT 9
US-09-734-673-3/c
; Sequence 3, Application US/09734673
; Patent No. 6410294
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001020
; CURRENT APPLICATION NUMBER: US/09/734,673
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38564
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3

Query Match 2.0%; Score 18; DB 4; Length 38564;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GTTCCTATTCTATGTGGT 323
Db 34622 GTTCCTATTCTATGTGGT 34605

RESULT 10
US-09-313-294A-940
; Sequence 940, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 940
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550095H1
US-09-313-294A-940

Query Match 1.9%; Score 17; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 TGATTCTGTGTCCTTC 597
Db 39 TGATTCTGTGTCCTTC 55

RESULT 11
US-09-833-381-1029/c
; Sequence 1029, Application US/09833381
; Patent No. 6672186

; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs.
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1029
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1029

Query Match 1.9%; Score 17; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 TGAGTGCCATGCTGCAC 288
Db 220 TGAGTGCCATGCTGCAC 204

RESULT 12
US-09-540-236-1026
; Sequence 1026, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1026
; LENGTH: 648
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1026

Query Match 1.9%; Score 17; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 TGCCAGTGTGGCATGT 418
Db 279 TGCCAGTGTGGCATGT 295

RESULT 13
US-09-540-236-1020/c
; Sequence 1020, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1020
; LENGTH: 801
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1020
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APPLICATION NUMBER: 07/635,475  
FILING DATE: 28-Dec-1990  
APPLICATION NUMBER: 07/377,238  
FILING DATE: 06-Jul-1984  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: TRV 2 005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 264 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Nucleotide-genomic DNA  
HYPOTHETICAL: Irrelevant  
ANTI-SENSE: Irrelevant  
SEQUENCE CHARACTERISTICS:  
FRAGMENT TYPE: Endonuclease restriction  
FRAGMENT TYPE: fragment  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: Irrelevant  
INDIVIDUAL ISOLATE: Irrelevant  
DEVELOPMENTAL STAGE: Irrelevant  
HAPLOTYPE: Irrelevant  
TISSUE TYPE: Lung  
CELL TYPE: Irrelevant  
CELL LINE: Irrelevant  
ORGANELLE: Irrelevant  
IMMEDIATE SOURCE:  
LIBRARY: Human genomic in lambda  
LIBRARY: FIX vector  
CLONE: F8  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: X  
MAP POSITION: q22  
UNITS: Irrelevant  
FEATURE:  
NAME/KEY: COL4A5 collagen gene  
LOCATION: Exon 16 region from 3',  
LOCATION: end of gene  
IDENTIFICATION METHOD: DNA sequencing  
OTHER INFORMATION: The sequence contains 100  
OTHER INFORMATION: nucleotides from intron 16 (lower case letters),  
OTHER INFORMATION: nucleotides exon 16 (capital letters) and 24  
OTHER INFORMATION: nucleotides of intron 15 (lower case letters).  
US-08-692-989-16  
Query Match 2.0%; Score 18; DB 4; Length 264;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 589 TTGGTCTTCAGGCTTC 606  
Db 212 TTGGTCTTCAGGCTTC 229  
RESULT 6  
US-09-328-352-3416  
Sequence 3416, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3416  
LENGTH: 684  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-3416  
Query Match 2.0%; Score 18; DB 4; Length 684;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 611 TTATGTTGATGGTGCGA 628  
Db 252 TTATGTTGATGGTGCGA 269  
RESULT 7  
US-09-252-991A-10198/c  
Sequence 10198, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 10198  
LENGTH: 1311  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10198  
Query Match 2.0%; Score 18; DB 4; Length 1311;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 84 TATTGGGGGCTGGTGGG 101  
Db 325 TATTGGGGGCTGGTGGG 308  
RESULT 8  
US-09-252-991A-9867  
Sequence 9867, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9867  
LENGTH: 4248  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9867  
Query Match 2.0%; Score 18; DB 4; Length 4248;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 84 TATTGGGGGCTGGTGGG 101



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 17:46:14 ; Search time 91 Seconds  
(without alignments)  
5598.296 Million cell updates/sec

Title: US-10-055-106C-1  
Perfect score: 918  
Sequence: 1 atgctggccacaatactc.....attgtgtttgtgcgcttag 918

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 12

Total number of hits satisfying chosen parameters: 30028

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19	2.1	263	4	US-09-016-434-168
2	19	2.1	433	3	US-09-171-410-2
3	19	2.1	5336	3	US-09-359-757-1
4	18	2.0	258	4	US-09-252-991A-10058
5	18	2.0	264	4	US-08-692-989-16
6	18	2.0	684	4	US-09-328-352-3416
7	18	2.0	1311	4	US-09-252-991A-10198
8	18	2.0	4248	4	US-09-252-991A-9867
9	18	2.0	38564	4	US-09-734-673-3
10	17	1.9	258	4	US-09-313-294A-940
11	17	1.9	472	4	US-09-833-381-1029
12	17	1.9	648	4	US-09-540-236-1026
13	17	1.9	801	4	US-09-540-236-1020
14	17	1.9	978	4	US-09-489-039A-1185
15	17	1.9	1057	4	US-09-833-381-461
16	17	1.9	1332	4	US-09-976-594-310
17	17	1.9	1761	3	US-09-033-055A-3
18	17	1.9	2098	2	US-08-937-931-5
19	17	1.9	2098	3	US-09-285-502-5
20	17	1.9	2098	4	US-09-709-126-5
21	17	1.9	2098	4	US-09-871-385A-5
22	17	1.9	2100	1	US-08-332-576-1
23	17	1.9	2100	5	PCT-US95-13672-1
24	17	1.9	2998	4	US-09-081-385-4
25	17	1.9	2998	4	US-09-081-385-149
26	17	1.9	3014	1	US-08-808-982-1
27	17	1.9	3014	3	US-09-306-902A-1

C 28	17	1.9	5280	4	US-08-956-171E-544
C 29	17	1.9	269223	4	US-09-596-002-41
C 30	17	1.9	269223	4	US-09-596-002-41
C 31	17	1.9	640681	4	US-09-790-988-1
C 32	17	1.9	786431	4	US-09-751-389-3
C 33	17	1.9	1664976	4	US-08-916-421B-1
C 34	17	1.9	1830121	4	US-09-557-884-1
C 35	17	1.9	1830121	4	US-09-643-990A-1
C 36	16	1.7	207	4	US-09-328-352-2491
C 37	16	1.7	288	4	US-09-313-294A-4045
C 38	16	1.7	366	4	US-09-621-976-9005
C 39	16	1.7	436	4	US-09-397-787-268
C 40	16	1.7	503	1	US-08-592-126-133
C 41	16	1.7	503	4	US-09-168-595-133
C 42	16	1.7	513	1	US-08-462-894-15
C 43	16	1.7	513	1	US-08-206-185-15
C 44	16	1.7	516	1	US-08-462-894-14
C 45	16	1.7	516	1	US-08-462-894-16

ALIGNMENTS

RESULT 1  
US-09-016-434-168  
; Sequence 168, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA: US/09/016,434  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 168:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRAINOT12  
; CLONE: 1413041  
; US-09-016-434-168

Query Match 2.1%; Score 19; DB 4; Length 263;  
Best Local Similarity 100.0%; Pred. No. 6.8;

Search completed: April 25, 2004, 22:26:10  
Job time : 94 secs

QY	216	LeuSerHisGlnGluPhe---TrrAlaGlnLeuLysAsnLeuPheHeileGlyValle	234
Db	694	TAACTAGACCAAAAATAAACAATGAAGTTTAAAAATGATTITGTACATTTCATC	753
QY	235	Leu-----ValCysPheLeuProTyrGlnPhePhearglleTyrTyrLeuAnVal	252
Db	754	ATATTCTGTTCTGTTTGTTCCTTACATATCAATCTTATTTATATCTTCTGTGAGA	813
QY	253	ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluLeuPheLeuSerVal	272
Db	814	ACACAACATTTGTTTAATGCTCAGTAGTGCGACGACTAGGCAATGTACCACATCACT	873
QY	273	ThralalleSer-----CysTyAspLeuLeuLeuPheValPhe	285
Db	874	CTCTGATTGCTGTTTCCAACTGTTGTTGGACCCCTATAGTTTACTACTTT	924
<b>RESULT 15</b>			
US-08-467-948A-7			
; Sequence 7, Application US/08467948A			
; Patent No. 5998184			
; GENERAL INFORMATION:			
; APPLICANT: LI, YI			
; APPLICANT: CAO, JIAN			
; APPLICANT: NI, JIAN			
; APPLICANT: GENTZ, REINER			
; APPLICANT: BULT, CAROL J.			
; APPLICANT: SUTTON III, GRANGER G.			
; APPLICANT: ROSEN, CRAIG A.			
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein			
; NUMBER OF SEQUENCES: 30			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.			
; STREET: 1100 NEW YORK AVE., NW, SUITE 600			
; CITY: WASHINGTON			
; STATE: DC			
; COUNTRY: USA			
; ZIP: 20005			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: FLOPPY DISK			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30			
; CURRENT APPLICATION DATA:			
; FILING DATE: 06-JUN-1995			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/467,948A			
; FILING DATE: 30-MAR-1995			
; REGISTRATION NUMBER: 36,688			
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 202-371-2600			
; TELEFAX: 202-371-2540			
; INFORMATION FOR SEQ ID NO: 7:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1301 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: both			
; TOPOLOGY: both			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 161..1192			
US-08-467-948A-7			
Alignment Scores:			
Pred. No.:	4,766-13	Length:	1301
Score:	217.00	Matches:	75
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QY	42	LeuValLysMetAsnThrArgSerValThrMetAlaValilleAsnLeuValVal	61
Db	172	ATCTCGCTCCCAAGTCGGAATCAAACCTACACTTACATGATTAACTTGGCAATGCA	231
QY	62	HisSerValPheLeuThrValProPheargLeuThrTyrLeuLysLysThrTrp	81
Db	232	GACTTGCCTTTGTTTACTTACCTTCCAGGATTTTTTACTTCAACACACGGAATGG	291
QY	82	MetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHsMetTyrLeu	101
Db	292	CATTTGGAGATTACTTTGTAAGATTCTGTGATGCTGTTTATACCAACATGATCGGA	351
QY	102	ThrPheLeuPheTyrValValilleLeuValThrArgTyrLeu---IlePhePheLysCys	120
Db	352	AGCATCTGTTCTTAACCTGATTAGTGTAGATGATTTCTGGCAATTTGCTACCCATTT	411
QY	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLaserAlaglyMetTrp	140
Db	412	RAGTCAAGACT--CTAAGAACCAAAAGAAATGCAAGATTGTTGCACTGGCGGTGG	468
QY	141	ThrLeuValilleValilleValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	469	TAACTGTGATCGGAGGAGTGCACCCGCCGTTTTTGTTCAG---TCTACCATCTTCAG	525
QY	161	TyrAsn-----GluGluHisCysPheLysPheHisLysGluLeuAlaTyr---ThrTyr	177
Db	526	GGTAAACATGCCTCAGAACCTGCTTTGAAATTTTCCAGAGGCCACATGGAAACATAT	585
QY	178	VallylIlelleAsnTyrMetIleValillePheValilleAlaValAlaValilleLeu---	196
Db	586	CTCTCA-----AGGATTGTAATTTTCATCGAAATAGTGGGATTTTTTATTCCT	633
QY	197	LeuValPheGlnValPheIlelleMetLeuMetValGlnLysLeuAtgHisSerLeu---	215
Db	634	CTAATTTAAATGTTGTTCTAGTATGGGTGCTAAATTTTAAACCAACCTGTTACA	693



[illegible]



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QY 37 SerIleLeuPheLeuValValMetAsnThrArgSerValThrMetAlaValle 56
Db 328 TATGTGATCTCGCTACGCGCAAGATGAAGACC-----GCTACCAACATCTACATCTTA 381
QY 57 AsnLeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu 76
Db 382 AACCTGCTATGTGTGATGAGAGCTGCTCATGCTCAGCGTGGCCCTTCTGGTCATCTCCAGC 441
QY 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 442 CTGTGTGGCCATCGCCCTTCGGCGCGCTACTTTGGCCCTGGTGCTCAGCGTGATGCG 501
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeuLe 116
Db 502 GTCACATGTTTCCACAGCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
QY 117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSer 136
Db 562 GTGTGTGACCCGATCAAGCAGCGCTACGCTGCGGCCCTGCTGGCGCAAGTAGTAGAAC 621
QY 137 AlaGlyMetTrpThrLeuValleValleValleValProLeuValVal----SerArgTyr 155
Db 622 CTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 681
QY 156 GlyIleHisGluGluTyrAsnGluLysHisCysPheLysPheHisLysGluLeuAlaTyr 175
Db 682 GCACCCACAGCGAT----GGCAGCGTAGCTGCAACATGCTCATGCGCGCGCGCGCGCGCAG 738
QY 176 ThrTyr---ValLysIleIleAsnTyrMetIleValle---PheValIleAlaValAla 193
Db 739 CGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 798
QY 194 ValIleLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuValGHis 213
Db 799 GCCATTTGCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
QY 214 SerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn----- 227
Db 841 --ATGGTGGCCCTCAAGCTGGCTGGCGAGCGCAAGCGCTCAGAGCGCAAGATCACT 897
QY 228 -----LeuPhePheIleGlyValleLeuValCysPheLeuProTyrGlnPhePhe 244
Db 898 CTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
QY 245 ArgIleTyrTyrLeuAsnVal----- 251
Db 952 GTGTGACAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1011
QY 252 -----ValThrHisSerAsnAlaCysAsnSerLysValAlaPhe----- 264
Db 1012 GTCATCTCGGCTATGCAACAGCTGTGCCAACCCCATCTCTACGGCTTCTCTGTCGGAC 1071
QY 265 --TyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAsp 279
Db 1072 AACTTCAGCGCTTTTCCAGCGCATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119

RESULT 11
US-07-816-283-1
; Sequence 1, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-1

Alignment Scores:
Pred. No.: 5 08e-13 Length: 1634
Score: 218.00 Matches: 72
Percent Similarity: 45.89% Conservative: 73
Best Local Similarity: 22.78% Mismatches: 121
Query Match: 13.69% Indels: 50
DB: 14 Gaps: 14

US-10-055-106C-2 (1-305) x US-07-816-283-1 (1-1634)
QY 2 ProGlyHisAsnThrSerArgAsnSerSer---CysAspProIleValThrProHisLeu 20
Db 220 CCAGGGCGAAATCGCTCCAGAACCGGACCTTGACGAGCGCGCGCGCGCGCGCGCGCGCGCG 279
QY 21 IleSer---LeuTyrPheIleValleLeuIleGlyLeuValGly-----Valle 36
Db 280 ATCTCTTTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 339
QY 37 SerIleLeuPheLeuValLysMetAsnThrArgSerValThrThrMetAlaValle 56
Db 340 TAGTGTATCTCGCTATGCCAAGATGAAGACG-----GCCACCAACATCTACATCTCTTA 393
QY 57 AsnLeuValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu 76
Db 394 ATCTGGCCATTCGTGATGAGTGTCTGCTCAGCTCAGCGTGGCTTCTTAGTACCTCCACG 453
QY 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 454 TTGTTGGCGCACTGGCCCTTCGCTGCGCTCTGCTGCGGCTCTGCTCAGCGTGACGCG 513
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeuLe 116
Db 514 GTCAACATGTTTCCACAGCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
QY 117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSer 136
Db 574 GTGTGTGATCCCATCAAGCGCGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 633
QY 137 AlaGlyMetTrpThrLeuValleValleValleValProLeuValVal----SerArgTyr 155
Db 634 CTGGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 693
QY 156 GlyIleHisGluGluTyrAsnGluLysHisCysPheLysPheHisLysGluLeuAlaTyr 175
Db 694 GCGGCCAACAGCGAC---GGCAGCGTGGCTTGCACATGCTCTATGCCAGAGCGCGCTCAA 750
QY 176 ThrTyr---ValLysIleIleAsnTyrMetIleValle---PheValIleAlaValAla 193
Db 751 CGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 810
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; LENGTH: 1265 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-816-283-3

Alignment Scores:
Pred. No.: 3 63e-13 Length: 1265
Score: 218.00 Matches: 72
Percent Similarity: 45.89% Conservative: 73
Best Local Similarity: 22.78% Mismatches: 121
Query Match: 13.69% Indels: 50
DB: 1 Gaps: 14

US-10-055-106C-2 (1-305) x US-07-816-283-3 (1-1265)
QY 2 ProGlyHisAsnThrSerArgAsnSerSer---CysAspProIleValThrProHisLeu 20
Db 208 CCTGGACGAAACGGCTTCCAGATGGAGCTTAAGCGAGGACAGGGTAGCCCATTTCTC 267
QY 21 IleSer---LeuTyrPheIleValLeuIleGlyLeuValGly-----ValIle 36
Db 268 ATCTCTTTTCATCTACTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327
QY 37 SerIleLeuPheLeuValIleValIleValIleValIleValIleValIleValIle 56
Db 328 TATGTGATCTCGCTACGCCAAGATGAAGACC-----GCTACCAACATCTACATTTCTA 381
QY 57 AsnLeuValValIleValIleValIleValIleValIleValIleValIleValIle 76
Db 382 AACCTGGCTATTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
QY 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 442 CTGTTGGCCACTGGCCCTTCGGCGGCTACTTTTGGCGGCTGCTGCTGCTGCTGCTGCTG 501
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValIleValIleValIleValIleValIle 116
Db 502 GTCAACATGTTTCCAGCATCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
QY 117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSer 136
Db 562 GTGGTGCCACCGCATCAAGCGCGCTACTCCGTCGCGCCACTGTGGCCAAAGTAGTGAC 621
QY 137 AlaGlyMetTrpThrLeuValIleValIleValIleValIleValIleValIleVal 155
Db 622 CTGGCGGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
QY 156 GlyIleHisGluLutyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyr 175
Db 682 GCAGCCAAACGCGAT---GGCAGCGGTAGCCTGCAACATGCTCATGCCGCGGCCAG 738
QY 176 ThrTyr---ValLysIleIleAsnTyrMetIleValIle---PheValIleAlaValAla 193
Db 739 CGCTGGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
QY 194 ValIleLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHis 213
Db 799 GCCATTGGCTGTGTTAT-----GTGCTCATCATTCGCAAGATGCGC--- 840
QY 214 SerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn----- 227
Db 841 ---ATGTGGCCCTCAAGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 897
QY 228 -----LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePhe 244
Db 898 CTAATGGTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 951
QY 245 ArgIleTyrTyrLeuAsnVal----- 251
Db 952 GTGGTACAGCTGTGTCAACGTTGTTGGCGGAGCAAGACGACGCCACCGTGGAGCCAGTTGTCT 1011
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Db 214 ATATGACTTACCTTCCGAATGTTTATATGCAAAAGATGCATGGCCATTTGGAGAG 273  
 Qy 86 ProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPhe 105  
 Db 274 TACTCTCGCCAGATTATTGGAGCTCTCACAGTGTCTTTTACCAAGCATTTCTTTATGGCTT 333  
 Qy 106 TyrValIleLeuValThrArgTyrLeuIlePhePheCysLysAspLysValGlu 125  
 Db 334 CTTCCTTTTATAGTGTGACATATAGTCCCATTTGTACAGCCGAGTACCCCAAGAA 393  
 Qy 126 PheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyrPheLeuValIleVal 145  
 Db 394 CTTAAACACAGTGCACAAAGCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 453  
 Qy 146 IleValValProLeuValSerArgTyrGlyIleHisIleGluTyrAsnGluHis 165  
 Db 454 ACGACACCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 513  
 Qy 166 CysPheLysPheHisLysGluLeuAlaTyrThrTyrValIleHisMetTyrMetIle 185  
 Db 514 TGCCTCAAGATTCTGACATCATC-----TATCTAAAGCTGTGAACGTGTGAAC 564  
 Qy 186 ValIlePheValIleAlaValAlaValIleLeuLeuValPheGlnValPheIleMet 205  
 Db 565 CTCACTCGATGACATTTTCTTGTATCTCTTGTCTCATGATGGTGTCTGTCTGTCTGT 624  
 Qy 206 LeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeu 225  
 Db 625 GTCAATTATCAATATCTCTTCAAGCAGGAGCTCTTAAGCTGAACCCCAAGTCAAGGAG 684  
 Qy 226 LysAsnLeuPhePheIleGlyVal-----IleLeuValCysPheLeuProTyr 241  
 Db 685 AAGTCCATAGGATCATCATCATC-----TATCTAAAGCTGTGAACGTGTGAAC 564  
 Qy 242 GlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSerLys 261  
 Db 745 CACATCTGT---TTCCGCTTCTCTGTGTGGAAACCGGGGAGAACAGTTACAACTCCCTGG 801  
 Qy 262 ValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeuLeu 281  
 Db 802 GGAGCCTTT-----ACCACCTTCTCTC---ATGAACCTCAGCAGCTGTGTGATGTGATT 852  
 Qy 282 LeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeu 298  
 Db 853 CTCTAC---TACATCGTTTCAAAACAATTTTCAGGCTCGAGTCAATAGTGTGC 900

## RESULT 7

US-09-170-496D-35  
 ; Sequence 35, Application US/09170496D  
 ; Patent No. 6553339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic P.  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Liaw, Chen W.  
 ; TITLE OF INVENTION: No. 6553339-Endogenous, Constitutively Activated Human G Protein-  
 ; TITLE OF INVENTION: Receptors  
 ; FILE REFERENCE: AREN-0040  
 ; CURRENT APPLICATION NUMBER: US/09/170,496D  
 ; CURRENT FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 294  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 35  
 ; LENGTH: 996  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-170-496D-35

Alignment Scores:  
 Pred. No.: 1,65e-13 Length: 996  
 Score: 220.00 Matches: 68  
 Percent Similarity: 44.11% Conservative: 63  
 Best Local Similarity: 22.90% Mismatches: 154  
 Query Match: 13.82% Indels: 12

DB: 4 Gaps: 6  
 US-10-055-106C-2 (1-305) x US-09-170-496D-35 (1-996)  
 Qy 6 ThrSerArgAsnSerSerCysAspProIleValThrProHisLeuIleSerLeuTyrPhe 25  
 Db 34 ACITTTAACAGCTCACATCCAGATGAATACAAATATGCAGCCCTTGTCTCTATAGCTGT 93  
 Qy 26 IleValLeuIleGlyLeuValGlyValIleSerIleLeuPheLeuLeuValIleMet 45  
 Db 94 ATCTTCAATATGATATTTTGTAACTACATCATGATTTGAGTTTTCAGTTGTACACACC 153  
 Qy 46 AsnThrArgSerValThrMetAlaValIleAsnLeuValValHisSerValPhe 65  
 Db 154 AAGAAGAGAACACCGTAAACCATCTATATGATGAATGTGGCATTAGTAGGACTTGATATT 213  
 Qy 66 LeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeu 85  
 Db 214 ATATGACTTTACCTTTTCGAATGTTTATATGCAAAAGATGCATGGCCATTTGGAGAG 273  
 Qy 86 ProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPhe 105  
 Db 274 TACTTCTGCAGATTATTGGAGCTCTCACAGTGTCTTACCAAGCATTTTATGGCTT 333  
 Qy 106 TyrValIleLeuValThrArgTyrLeuIlePhePheLysCysLysAspLysValGlu 125  
 Db 334 CTTCGCTTTTATAGTGTGACATCATGATGGCATTGTACAGCCGAGTACCCCAAGAA 393  
 Qy 126 PheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyrLeuValIleVal 145  
 Db 394 CTTAAACACAGTGCACAAAGCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 453  
 Qy 146 IleValValProLeuValSerArgTyrGlyIleHisGluGluTyrAsnGluHis 165  
 Db 454 ACGACACCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 513  
 Qy 166 CysPheLysPheHisLysGluLeuAlaTyrThrTyrValIleHisMetTyrMetIle 185  
 Db 514 TGCCTCAAGATTCTGACATCATC-----TATCTAAAGCTGTGAACGTGTGAAC 564  
 Qy 186 ValIlePheValIleAlaValAlaValIleLeuLeuValPheGlnValPheIleMet 205  
 Db 565 CTCACTCGATGACATTTTCTTGTATCTCTTGTCTCATGATGGTGTCTGTCTGTCTGT 624  
 Qy 206 LeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeu 225  
 Db 625 GTCAATTATCAATATCTCTTCAAGCAGGAGCTCTTAAGCTGAACCCCAAGTCAAGGAG 684  
 Qy 226 LysAsnLeuPhePheIleGlyVal-----IleLeuValCysPheLeuProTyr 241  
 Db 685 AAGTCCATAGGATCATCATCATC-----TATCTAAAGCTGTGAACGTGTGAAC 744  
 Qy 242 GlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSerLys 261  
 Db 745 CACATCTGT---TTCCGCTTCTCTGTGTGGAAACCGGGGAGAACAGTTACAACTCCCTGG 801  
 Qy 262 ValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeuLeu 281  
 Db 802 GGAGCCTTT-----ACCACCTTCTCTC---ATGAACCTCAGCAGCTGTGTGATGTGATT 852  
 Qy 282 LeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeu 298  
 Db 853 CTCTAC---TACATCGTTTCAAAACAATTTTCAGGCTCGAGTCAATAGTGTGC 900

## RESULT 8

US-08-417-103-13  
 ; Sequence 13, Application US/08417103  
 ; Patent No. 5723299  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bell, Graeme I.  
 ; APPLICANT: Yamada, Yuichiro  
 ; APPLICANT: Seino, Susumu  
 ; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

1130 ---TTAAGGACAGACTA 1144

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Db 991 TGTTACATAGCCATA-----TCAGGTACATCCCAAAATCCAGC 1029
Qy 219 GlnGluPheTrpAlaGlnLeuLysAsn-----LeuPhePhe 230
Db 1030 AGGCAATTCAATGATCAGTCAAGCGGAAAGCGAAACATACACAGAGCATCAGGGTTGTT 1089
Qy 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle----- 246
Db 1080 GTGGGTGTGATTTTACCTGCTTTTACCATATACATCTGTGCGAGATGCCCTTCTACTTTT 1149
Qy 247 TyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyr--- 265
Db 1150 AGTCACCTTAGACAGCGCTTTTAGATCAATCTGCA-----CAAAAATCTATATCTACTG 1203
Qy 266 AsnGluIlePheLeuSerValThrAlaIleSer---CysTyrAspLeuLeuVal 284
Db 1204 AAAGAAATACACTTTTCTGTCTGCGTGAATGTTTSCCTGGATCCCAATATTTACTTT 1263
Qy 285 Phe-----GlyGlySerHisTrpPheLysGlnLys 294
Db 1264 TTCATGTGTAGTCACTTTTCAAGATGGCTGTTCAAAAAA 1302

RESULT 4
US-09-919-172-21
; Sequence 21, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1650519CB1
US-09-919-172-21

Alignment Scores:
Pred. No.: 2,03e-14 Length: 1444
Score: 231.00 Matches: 76
Percent Similarity: 43.13% Conservative: 59
Best Local Similarity: 24.28% Mismatches: 144
Query Match: 14.51% Indels: 34
DB: 4 Gaps: 10

US-10-055-106C-2 (1-305) x US-09-919-172-21 (1-1444)
Qy 2 ProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeuIle 21
Db 406 CCAGGAAAGAACACACCCCTTCAAGATGTTGACACATTTGCTTGGCGGTCTTTAT 465
Qy 22 SerLeuTyrPheIle-----ValLeuIleGlyGlyLeuValGlyValIleSerIleLeu 39
Db 466 CTCATTATATTGTCGCAAGCATCTTGTCTGAATGGTTTAGCA-----GTG 510
Qy 40 PheLeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 59
Db 511 TGGATCTTCTTCACATAGGATATAAACACGCTTATATCTTATCTCAAAACATAGTG 570
Qy 60 ValValHisSerValPheLeuThrValProPheArgLeuThrTyrLeuLys---- 78
Db 571 GTTCGACACCTCATATATGAGCTTGACATTTCCATTTCCGATAGTCCATGATGAGGATTT 630
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Qy 79 LysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHis 98
Db 631 GGACCTTGGTACTCAAGTTTATTTCTGCAGATACACTTCAGTTTGTGTTTATGCAAC 690
Qy 99 MetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePhe 118
Db 691 ATGTATACTTCCATCGTGTCTTGGCTGATAGCAATGATCGCTATCTGAAGGTGGTC 750
Qy 119 LysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGly 138
Db 751 AAGCCATTTGGGACTCTCGGATGTACAGCATAACCTTCACGAAGGTTTTATCTGTTGT 810
Qy 139 MetTrpThrLeuValIleValValValProLeuValValSerArgTyrGlyIleHis 158
Db 811 GTTGGGTGATCACTGCTGTTTGTGCGCGTCTGCTGTGATTTCTGATCGGA 870
Qy 159 GluGluTyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVal 178
Db 871 ACAGAGGACAATATCCATGACTGCTCAAAACTTAAAGTCTTTGGGGGTCAAAATGGCAT 930
Qy 179 LysIleIleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuVal 198
Db 931 ACGGAGTCCACCTATGTGAACAGCTGCTGTTTGTGCGCGTCTGCTGTGATTTCTGATCGGA 990
Qy 199 PheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHis 218
Db 991 TGTTACATAGCCATA-----TCCAGGTACATCCACAAATCCAGC 1029
Qy 219 GlnGluPheTrpAlaGlnLeuLysAsn-----LeuPhePhe 230
Db 1030 AGGCAATTCAATGATCAGTCAAGCGGAAAGCGAAACATACACAGAGCATCAGGGTTGTT 1089
Qy 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle----- 246
Db 1090 GTGGGTGTGATTTTACCTGCTTTTACCATATACATCTTGTGCGAGATGCCCTTCTACTTTT 1149
Qy 247 TyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyr--- 265
Db 1150 AGTCACCTTAGACAGCGCTTTTAGATGAATCTGCA-----CAAAAATCTTATATTTACTGC 1203
Qy 266 AsnGluIlePheLeuSerValThrAlaIleSer---CysTyrAspLeuLeuVal 284
Db 1204 AAAGAAATACACTTTTCTGTCTGCGTGAATGTTTSCCTGGATCCCAATATTTACTTT 1263
Qy 285 Phe-----GlyGlySerHisTrpPheLysGlnLys 294
Db 1264 TTCATGTGTAGTCACTTTTCAAGATGGCTGTTCAAAAAA 1302

RESULT 5
US-09-585-876-1
; Sequence 1, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205e1 GPCR-Like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(1237)
US-09-585-876-1
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/ REFERENCE/DOCKET NUMBER: GH-70001-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1578 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-044-404A-1

Alignment Scores:
Pred. No.: 2,76e-15 Length: 1578
Score: 240.00 Matches: 67
Percent Similarity: 48.06% Conservative: 82
Best Local Similarity: 21.61% Mismatches: 133
Query Match: 15.08% Indels: 28
DB: 3 Gaps: 11

US-10-055-106C-2 (1-305) x US-09-044-404A-1 (1-1578)
QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 479 GGAATCTGCAGATATCTCTGCACATGCCATGACACTATTGATGACTTCCGCAATCAA 538
QY 19 HisLeuIleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
DB 539 GTGTATTCACCTTGACTGATGATCTCTGTGTAGGCTTCTTGGCAGTGGCTTTGGT 598
QY 39 LeuPheLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
DB 599 CTCTATGCTCTATAAAACCTATCAAGAAGTCAGCCTTCCAAAGTATACATGATTAAT 658
QY 58 LeuValValValHisSerValPheLeuThrValProPheArgLeuThrTyLeuIle 77
DB 659 TTAGCAGTAGCAGATCTATTGTGTGTGCACACTGCCTCTCCGTGTGTCTATTATGTC 718
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 719 CACAAAGGCATTGGCTTTGGTGACTTCTGTGGCGCCTCAGCACCTATGCTTTGTAT 778
QY 97 IleHisMetLeuThrPheLeuPheValValIleLeuValThrArgTyLeuIle 116
DB 779 GTCAACCTCTATTGTAGCATCTCTTTATGACAGCC-----ATGAGC 820
QY 117 PhePheLysCys-----LysAspLysValGluPheTyArgLysLeu 130
DB 821 TTTTCCGGTGCAATGCAATGTTTTCAGTCCAGAACATTAATTGGTTACACAGAA 880
QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValProLeu 150
DB 881 AAAGCCAGGTTTGTGTGTGTAGTATTGTGATTTTGTGATTTGACCAAGTTCTCCATT 940
QY 151 ValValSerArgTyGlyIleHisGluGluTyAsnGluHisCysPheLysPheHis 170
DB 941 CTAATGCCCAA---CCACAAAGATGGGAAATAATACCAAGTCTTGAGCCCCCA 997
QY 171 LysGlu---LeuAlaTyThrTyValLysIleIleAsnTy-----MetIleValIle 187
DB 998 CAAGACAATCAAACTAAAAATCATGTTTGTGTCTTCGATTTATGTCATTGTTGTGGC 1057
QY 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
DB 1058 TTTATCATCCTTTGTTATTAATGTTCTGTGTACATGATCATTTGACCTTACTA 1117
QY 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLysAsn 227
DB 1118 AAAAAATCAATGAAAAAATCTGTCAAGTCATAAAAAGGCTATGAAGATGATC----- 1171
QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyTrpGlnPheArgIleTy 247

REFERENCE/DOCKET NUMBER: GH-70001-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1578 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-044-404A-1

Alignment Scores:
Pred. No.: 2,76e-15 Length: 1578
Score: 240.00 Matches: 67
Percent Similarity: 48.06% Conservative: 82
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Query Match: 15.08% Indels: 28
DB: 3 Gaps: 11

US-10-055-106C-2 (1-305) x US-09-044-404A-1 (1-1578)
QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 479 GGAATCTGCAGATATCTCTGCACATGCCATGACACTATTGATGACTTCCGCAATCAA 538
QY 19 HisLeuIleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
DB 539 GTGTATTCACCTTGACTGATGATCTCTGTGTAGGCTTCTTGGCAGTGGCTTTGGT 598
QY 39 LeuPheLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
DB 599 CTCTATGCTCTATAAAACCTATCAAGAAGTCAGCCTTCCAAAGTATACATGATTAAT 658
QY 58 LeuValValValHisSerValPheLeuThrValProPheArgLeuThrTyLeuIle 77
DB 659 TTAGCAGTAGCAGATCTATTGTGTGTGCACACTGCCTCTCCGTGTGTCTATTATGTC 718
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 719 CACAAAGGCATTGGCTTTGGTGACTTCTGTGGCGCCTCAGCACCTATGCTTTGTAT 778
QY 97 IleHisMetLeuThrPheLeuPheValValIleLeuValThrArgTyLeuIle 116
DB 779 GTCAACCTCTATTGTAGCATCTCTTTATGACAGCC-----ATGAGC 820
QY 117 PhePheLysCys-----LysAspLysValGluPheTyArgLysLeu 130
DB 821 TTTTCCGGTGCAATGCAATGTTTTCAGTCCAGAACATTAATTGGTTACACAGAA 880
QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValProLeu 150
DB 881 AAAGCCAGGTTTGTGTGTGTAGTATTGTGATTTTGTGATTTGACCAAGTTCTCCATT 940
QY 151 ValValSerArgTyGlyIleHisGluGluTyAsnGluHisCysPheLysPheHis 170
DB 941 CTAATGCCCAA---CCACAAAGATGGGAAATAATACCAAGTCTTGAGCCCCCA 997
QY 171 LysGlu---LeuAlaTyThrTyValLysIleIleAsnTy-----MetIleValIle 187
DB 998 CAAGACAATCAAACTAAAAATCATGTTTGTGTCTTCGATTTATGTCATTGTTGTGGC 1057
QY 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
DB 1058 TTTATCATCCTTTGTTATTAATGTTCTGTGTACATGATCATTTGACCTTACTA 1117
QY 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLysAsn 227
DB 1118 AAAAAATCAATGAAAAAATCTGTCAAGTCATAAAAAGGCTATGAAGATGATC----- 1171
QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyTrpGlnPheArgIleTy 247
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 25, 2004, 20:06:25 ; Search time 87 Seconds

(without alignments)  
1945.517 Million cell updates/sec

Title: US-10-055-106C-2

Perfect score: 1592

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO.spool/US10055106/runat 21042004 161132 26207/app query.fasta 1.455  
-DB=Issued Patents NA -QWTF=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humans40.cdi  
-LIST=45 -LOCAL=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-USER=US10055106 -CGN 1 1.56 @runat 21042004 161132 26207 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	240	15.1	1578	3	US-09-044-404A-1
2	240	15.1	1578	4	US-09-586-924-1
3	231	14.5	1444	3	US-08-988-876-4
4	231	14.5	1444	4	US-09-919-172-21
5	223	14.0	1401	4	US-09-585-876-1
6	220	13.8	993	4	US-09-016-434-1064
7	220	13.8	996	4	US-09-170-496D-35
8	218	13.7	1205	1	US-08-417-103-13
9	218	13.7	1265	1	US-07-816-283-3
10	218	13.7	1265	1	US-08-417-103-3
11	218	13.7	1634	1	US-07-816-283-1
12	218	13.7	1634	1	US-08-417-103-1

#### ALIGNMENTS

##### RESULT 1

US-09-044-404A-1  
; Sequence 1, Application US/09044404A  
; Patent No. 6200775  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: HALSEY, WENDY  
; APPLICANT: ELLIS, CATHERINE  
; APPLICANT: AMES, ROBERT  
; APPLICANT: FOLEY, JAMES  
; APPLICANT: SARAU, HENRY  
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES  
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 790 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/044,404A  
; FILING DATE: MARCH 19, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/844,795  
; FILING DATE: APRIL 22, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T.  
; REGISTRATION NUMBER: 34,344

Sequence 1302, Ap  
Sequence 750, Ap  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 11, Appl  
Sequence 169, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1479, Ap  
Sequence 181, Ap  
Sequence 183, Ap  
Sequence 1270, Ap  
Sequence 1484, Ap  
Sequence 43, Ap  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1190, Ap  
Sequence 1021, Ap  
Sequence 1, Appli  
Sequence 1247, Ap  
Sequence 1, Appli  
Sequence 1426, Ap  
Sequence 31, Appl  
Sequence 7, Appli  
Sequence 1, Appli  
Sequence 717, Ap

13 218 13.7 1634 4 US-09-016-434-1302  
14 217 13.6 1140 4 US-09-016-434-750  
15 217 13.6 1301 2 US-08-467-948A-7  
16 217 13.6 1301 3 US-08-467-947A-7  
17 214 13.4 987 4 US-09-170-496D-11  
18 214 13.4 987 4 US-09-170-496D-169  
19 214 13.4 1027 3 US-09-303-524A-1  
20 214 13.4 1054 1 US-08-148-215A-1  
21 214 13.4 1596 4 US-09-016-434-1479  
22 214 13.4 2416 4 US-09-016-434-1270  
23 213 13.4 996 4 US-09-170-496D-183  
24 211 13.3 1020 4 US-09-170-496D-181  
25 208.5 13.1 1900 4 US-09-016-434-1484  
26 208.5 13.1 1901 1 US-08-153-848-43  
27 208.5 13.1 1901 3 US-09-299-843A-43  
28 208.5 13.1 1901 4 US-09-088-337B-43  
29 208.5 13.1 1901 5 PCT-US93-11153-43  
30 208.5 13.1 2453 5 PCT-US95-07180-1  
31 208 13.1 1143 1 US-08-467-125-1  
32 208 13.1 1143 2 US-08-911-320A-1  
33 208 13.1 1143 3 US-09-217-101-1  
34 208 13.1 1842 4 US-09-016-434-46  
35 206.5 13.0 1495 4 US-09-016-434-1190  
36 206.5 13.0 1495 4 US-09-023-655-1021  
37 206.5 13.0 2156 1 US-08-012-988A-1  
38 205 12.9 1068 4 US-09-023-655-1247  
39 205 12.9 1438 4 US-09-170-496D-1  
40 205 12.9 1438 4 US-09-016-434-1426  
41 204 12.8 1020 4 US-09-170-496D-31  
42 203.5 12.8 1244 1 US-07-816-283-7  
43 203.5 12.8 1244 1 US-08-417-103-7  
44 203.5 12.8 1640 3 US-08-781-250-1  
45 203 12.8 1236 4 US-09-016-434-717

**AUTHORS** GRASP Consortium, Davidson, W.S., Koop, B.F. and  
<http://web.uvic.ca/cbr/grasp>.  
**TITLE** A survey of Salmo salar transcripts from high complexity cDNA  
 libraries  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Koop BF  
 Centre for Biomedical Research  
 University of Victoria  
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
 Tel: 250 472 4067  
 Fax: 250 472 4075  
 Email: bkoop@uvic.ca  
 Genome Sciences Centre, BC Cancer Agency cDNA preparation,  
 sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J  
 Asano, N Ginn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D  
 Smalius, L Spence, J Scott, G Taylor, G Yang, J Schein, S Jones and  
 M Marra.

**FEATURES** Location/Qualifiers  
 source 1..648  
 /organism="Salmo salar"  
 /mol\_type="mRNA"  
 /strain="McConnell"  
 /db\_xref="taxon:8030"  
 /clone\_lib="mixed tissue"  
 /note="vector: pCMVSPORT6; Library Creator: Research  
 Genetics; Atlantic salmon tissue contributors: Carlo  
 Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),  
 Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery  
 (Crofton, B.C.), Rachel Roper (University of Victoria)"

**ORIGIN**

Alignment Scores:					
Pred. No.:	5.82e-18	Length:	648		
Score:	261.00	Matches:	51		
Percent Similarity:	59.84%	Conservative:	25		
Best Local Similarity:	40.16%	Mismatches:	31		
Query Match:	16.39%	Indels:	20		
DB:	14	Gaps:	2		

US-10-055-106C-2 (1-305) x CB514250 (1-648)

Qy	178	VallysllelleleantyrMetlleVallePheValleAlaValAlaValilleLeuLeu	197
Db	616	GTCAAGGTGCTGAACACTACATCAGCTCTGTGATCATCATTTGGCCTGTGTGCTGACG	557
Qy	198	ValPheGlnValPheilleMetleuMetValGlnLysLeuArgHisSerLeuLeuSer	217
Db	556	GCACCTGCAGTGTCTATGTCATGCTCTCTCCACAGGAAGTATGGCGGAGACTGCATGCT	497
Qy	218	HisGlnluPheTrpAlaGlnLeuLysAsnLeuPhePheilleGlyValilleLeuValCys	237
Db	496	CACCAGAGTCTGGGCTCAGCTGAGAGCCTGTGTTTGGTGTGCTGTGCTGTGTGT	437
Qy	238	PheLeuProTyrGlnPhePheArgileTyrTyrLeuAsnValValThrHisSerAsnAla	257
Db	436	TTTGTCCTCATACACGTTTCAGGATGATCTACCTGGACACCTGTACTGGAGACACT	377
Qy	258	CysAsnSerLysValAlaPheTyrAsnGluillePheLeuSerValThrAlaIleSerCys	277
Db	376	-----AACGAGGTATTCTCTCAGTCTCAGCGCCCTCAGCTGT	341
Qy	278	TyrAspLeuLeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysilleGly	297
Db	340	TTTGACATGCTTACTTTC-----CTAGGG	317
Qy	298	LeuTrpAsnCysValLeuCys	304
Db	316	AGGGGACACTGCTATATGTGT	296

Search completed: April 25, 2004, 22:16:30  
 Job time : 2909 secs



polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

## ORIGIN

Alignment Scores:  
Pred. No.: 3,166-25 Length: 679  
Score: 328.00 Matches: 56  
Percent Similarity: 63.74% Conservative: 50  
Best Local Similarity: 36.26% Mismatches: 62  
Query Match: 20.60% Indels: 4  
DB: 14 Gaps: 3

US-10-055-106C-2 (1-305) x CD469227 (1-679)

Qy 109 l l e l e u v a l t h r a r g t y r l e u l l e p h e p h e l y s c y s l y s a s p l y s a l g l u p h e t y r a r g 128  
Db 2 a t t g c a t a t t c c g a t t g c t a t c t a t t t t a a g --- a a a c t c c a c t g c a c a c a g t t a a a 58  
Qy 129 l y s l e u h i s a l a v a l a a l a s e r a l a g l y m e t t h r l e u v a l l e v a l l e v a l v a l 148  
Db 59 a a g t a c c a t g c g g t a g t t t a a g c a t t a t t t g g a t a g t g g t a g c t t a t t t t t t g 118  
Qy 149 p r o l e u v a l v a l s e r a r g t y r g l y l e h i s g l u g l u t y r a s n g l u --- g l u h i s c y a p h e 167  
Db 119 c c a a t a t t t t t t a c t a t a t g g c a a g a g t a c a a g t t a c t a g a a c a c a c a g a t g c t t 178  
Qy 168 l y s p h e h i s l y s g l u l e u a l a t y r t h r t y r v a l l y s l l e l l e a s n t y r m e t l e v a l l e 187  
Db 179 g a g t t c t a c a a g a c t t c a a c c a c a g g a a t t c a t c a t t t g a a t t a c t a t c t a t g a t t g c c 238  
Qy 188 p h e v a l l e a l a v a l a l e u l e u v a l p h e g l n v a l p h e l l e l l e m e t l e u m e t 207  
Db 239 a t t a t g a t g a c a g t g g t g a c c c t c t t c t g a t a c a g a t g g g t g c t a t t g t t c a a c t c 298  
Qy 208 v a l g l n l y s l e u a r g h i s e r l e u l e u s e r h i s g l n g l u p h e t r p a l a g l n l e u l y s a s n 227  
Db 299 a t a r a g g t t c t t g c c t g a c c t g t g g g c t c a t c a a g a g a t a t a g a c t c a a a t c a a g a g c 358  
Qy 228 l e u p h e p h e l l e g l y v a l l e l e u v a l c y s p h e l e u p r o t y r g l n p h e p h e a r g l l e t y r 247  
Db 359 t g c t t c t c c t t a g t a t a g t c g t c t g t t a t a c c c a c c a t g a t c c g g t a c a c 418  
Qy 248 t y r l e u a s n v a l v a l t h r h i s e r a s n a l a c y s a s n s e r l y s v a l a l a p h e t y r a s n g l u 267  
Db 419 t t t c t t c a g --- a a t a t t c a g g g a g a a a t t c t g a t a g t t c t t t a t a a t g a a 472  
Qy 268 l l e p h e l e u s e r v a l t h r a l a l e s e r c y s t y r a s p l e u l e u l e u p h e p h e g l y c l y 287  
Db 473 a t t t t g t g g t t t a a c t a c t g t c t g t t g c c t g g a t a g c t g t g t t c t a g t g g a g t t 532  
Qy 288 s e r h i s 289  
Db 533 a t c c a t 538

RESULT 12  
LOCUS CD699779 499 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST16303 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD699779  
VERSION CD699779.1 GI:32229387  
KEYWORDS EST.

SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 499)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsums.edu.cn.

## FEATURES

source  
1. 499  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

## ORIGIN

Alignment Scores:  
Pred. No.: 7,046-24 Length: 499  
Score: 314.00 Matches: 63  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.72% Indels: 0  
DB: 14 Gaps: 0  
US-10-055-106C-2 (1-305) x CD699779 (1-499)  
Qy 1 M e t P r o G l y H i s A s n T h r S e r A r g A s n S e r S e r C y s A s p P r o l l e v a l T h r P r o H i s L e u 20  
Db 311 A T C C T G C G C A C A A T A C C T C C A G A A T T C T C T T G C G A T C C T A T A G T A G C A C C C A C T T A 370  
Qy 21 I l e S e r L e u T y r P h e l l e V a l l e u l l e G l y G l y L e u V a l g l y V a l l e S e r l l e L e u P h e 40  
Db 371 A T A G C C T C T A C T T C A T A G T G C T T A T T G C G G C T G T G G T G T C A T T T C C A T C T T T T C 430  
Qy 41 L e u L e u V a l l y s M e t A s n T h r A r g S e r V a l T h r M e t A l a V a l l e A s n L e u V a l v a l 60  
Db 431 C T C C T G T G A A A T G A A C A C C C G G T C A G T C A C C A C C A T G C G G T C A T T A A C T T G T G T G 490  
Qy 61 V a l H i s S e r 63  
Db 491 G T C C A C A G C 499

RESULT 13  
LOCUS BG145683 478 bp mRNA linear EST 01-FEB-2001  
DEFINITION MAC33C07.Y1 Soares mouse 3N3MS Mus musculus cDNA clone  
IMAGE:4001652 5', mRNA sequence.

ACCESSION BG145683  
VERSION BG145683.1 GI:12649019  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-femail.nih.gov  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:1499380  
Seq primer: -40RP from Gibco  
High quality sequence stop: 392.

FEATURES  
source  
1. 478  
Location/Qualifiers  
/organism="Mus musculus"



Qy 218 sGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPh 238  
 Db 672 TCAAGAGTCTTGCGCACCATCGAAGATGTGTTTCTCTGGTGTATGTTTGTGTTT 731  
 Qy 238 eLeuProTyrGlnPhePheArgIleTyr 247  
 Db 732 TGTGCCCTATCAGGATTCAGAGTGAT 759

RESULT 8  
 AJ455645 834 bp mRNA linear EST 22-APR-2002  
 LOCUS AJ455645 riken1 Gallus gallus cdna clone 6b4r1, mRNA sequence.  
 DEFINITION AJ455645  
 ACCESSION AJ455645  
 VERSION AJ455645.1 GI:20265741  
 KEYWORDS EST  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 834)  
 AUTHORS Buerstedde J.M.  
 TITLE Gallus gallus bursal lymphocyte EST  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Buerstedde JM  
 Cellular Immunology  
 Heinrich-Pette-Institute  
 Martinistr. 52, 20251 Hamburg, Germany  
 Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES  
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 /cell\_type="bursal lymphocyte"  
 /dev\_stage="2-3 weeks old"  
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 /note="CB inbred strain"

ORIGIN  
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 Pred. No.: 1,43e-29 Length: 834  
 Score: 369.00 Matches: 72  
 Percent Similarity: 76.72% Conservative: 17  
 Best Local Similarity: 62.07% Mismatches: 26  
 Query Match: 23.18% Indels: 1  
 DB: 9 Gaps: 0

US-10-055-106C-2 (1-305) x AJ455645 (1-834)

Qy 20 LeuIleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeu 39  
 Db 439 CTGATTACTGTCTACTCAGTTCGCTTGTCTGGAGGTGGATGATCCATCGCAATGTC 498  
 Qy 40 PheLeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal 59  
 Db 499 TTGTGCTGTCTCAGATGAACAGTCTGTCTGTACCACTACAGCCAAATATCTAGTT 558  
 Qy 60 ValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLys 79  
 Db 559 GTGGTACATGCTCTCTCTCTCCACAGTGCCTTCGCTGTGCACTACTATGTCAAATAG 618  
 Qy 80 ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMet 99  
 Db 619 GAGTGGATCTTCCACATACCAATCTGTGNAATGTGTGATGTGTATGGTGCACATCCATG 678  
 Qy 100 TyrLeuThrPheLeuPheTyrValIleLeuValThrArgTyrLeu-IlePhePhe 119  
 Db 679 TATTGACTTTCTTCTTCTACCTGATCACATGCTGTGATCCGGNGGNTGGGCTTCTTTCA 738  
 Qy 119 sCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAla 134

Db 739 ATGAAGACAGCAGTAGAGTTTATAGAAAGCTNCATGCCATTGCT 784

RESULT 9  
 CA355790 680 bp mRNA linear EST 05-NOV-2002  
 LOCUS 627748 NCCWA 1RT Oncorhynchus mykiss cdna clone 1RT8K09\_A\_F05 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CA355790  
 VERSION CA355790.1 GI:24600977  
 KEYWORDS EST  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 REFERENCE 1 (bases 1 to 680)  
 AUTHORS Rexroad,C.E. and Keeler,J.W.  
 TITLE Sequence analysis of a rainbow trout normalized cDNA library  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified by  
 cross\_match v0.990329.  
 Seq primer: AGCGGATAACAAATTCACACAGGA.

FEATURES  
 Location/Qualifiers  
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 /db\_xref="taxon:8022"  
 /clone="1RT8K09\_A\_F05"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="NCCWA 1RT"  
 /note="Vector: PCMV SPORF6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from brain, gill, liver,  
 spleen, muscle, and kidney."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,24e-29 Length: 680  
 Score: 368.50 Matches: 69  
 Percent Similarity: 69.28% Conservative: 37  
 Best Local Similarity: 45.10% Mismatches: 44  
 Query Match: 23.15% Indels: 3  
 DB: 14 Gaps: 2

US-10-055-106C-2 (1-305) x CA355790 (1-680)

Qy 9 AnSerSerCysAspProIleValThrProHisLeuIleSerLeuTyrPheIleValLeu 28  
 Db 223 AACTCTACCATCTCCACCTCAACCTCTTACCCCTGTGTCCATCTATAGCTGTCTCTG 282  
 Qy 29 IleGlyGlyLeuValGlyValIleSerIleLeuPheLeuValLysMetAsnThrArg 48  
 Db 283 GTCATTGGGGTCAATCGG---TTGGCCCTGATGATCCACATCTCCATCCACATGCG 339  
 Qy 49 SerValThrThrMetAlaValIleAsnLeuValValHisSerValPheLeuLeuThr 68  
 Db 340 TCAGTTATCACCATCGCTATGCTCAACCTCACTGGCCCACTTCTCTTCTACTCACC 399  
 Qy 69 ValProPheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeuProPheCys 88  
 Db 400 GTACCCCTTCAGGATCTACTACTATGCTGTGTGTGTTTGGGGAGATGCTGTGT 459  
 Qy 89 LysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPheTyrValVal 108  
 Db 460 AAGNGGTCAGTGCCCATGATCCACGTCGACATGTATACGCTTGTGTTTCTTACGCTGTC 519



/clone="IMAGE:4917024"

/tissue type="tumor, gross tissue"

/dev stage="5 months"

/lab host="DH10B"

/clone lib="NCI CGAP Mam4"

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model; Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

# ORIGIN

Alignment Scores:  
Pred. No.: 2,538-43 Length: 646  
Score: 494.00 Matches: 97  
Percent Similarity: 90.27% Conservative: 5  
Best Local Similarity: 85.84% Mismatches: 11  
Query Match: 31.03% Indels: 0  
DB: 12 Gaps: 0

US-10-055-106c-2 (1-305) x BG862323 (1-646)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20  
DB 307 ATGGATGGATATAATACCTCTGAGATTCTCTGTGACCTATATCTGGCACCACTTA 366  
QY 21 IleSerLeuTyrPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40  
DB 367 ACATCGATTACTTCATAGTCTGATGGAGACTGGTAGGCTCATCTCCATCCGGTTC 426  
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60  
DB 427 TTGCTGGTGAATGAATCACTCAGTTCAGTGACCACTGGCTGTATCAACCTCGTGTG 486  
QY 61 ValHisSerValPheLeuLeuThrValPropheArgLeuThrTyrLeuIleIleValThr 80  
DB 487 GTTCATGGGCTCTCTACTGACGGTCCCTTCGCTGGCATCTCATCAAGGGACT 546  
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100  
DB 547 TCGACGTTTGATTTACCTCTTGCAAAATTTGAGTGCCATGTTACATATCCACATGTAC 606  
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArg 113  
DB 607 CTCACGTTCTCTTCTACGTGGTGATCTAGTCATCAGA 645

# RESULT 7

CA965628 844 bp mRNA linear EST 03-JAN-2003  
LOCUS CcLX05a15h17f1 Carp mixed tissue library 2 Cyprinus carpio cDNA  
DEFINITION clone 15h17 5', mRNA sequence.

ACCESSION CA965628

VERSION 1 GI:27492185

KEYWORDS EST.

SOURCE Cyprinus carpio (common carp)

# ORGANISM

Cyprinus carpio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Cyprinus.

1. (bases 1 to 844)

Gracey A.V., Fraser E., Li W. and Cossins, A.R.

Microarray and EST analysis of the carp (Cyprinus carpio)

transcriptome during environmental stress

Unpublished (2003)

Contact: Andrew R. Cossins

Laboratory for Environmental Gene Regulation

University of Liverpool

School of Biological Sciences, The Biosciences Building, Crown

Street, Liverpool, United Kingdom, L69 7ZS

Tel: +44(0)151-795-4510

Fax: +44(0)151-795-4431

Email: cossins@liv.ac.uk

Vector has been trimmed from this EST.

Plate: 15 row: h column: 17

Seq primer: TripleX 5' LD (5'-CTCGGGAAGCGGCCATTGTGTGT-3')

High quality sequence start: 39

High quality sequence stop: 580.

# FEATURES

Location/Qualifiers  
1..844  
/organism="Cyprinus carpio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7962"  
/clone="15h17"  
/sex="Male & female"  
/tissue type="Skeletal white muscle, cardiac muscle,  
kidney, brain, gill, intestinal mucosa"  
/dev stage="Adult"  
/lab host="E.coli Electromax DH10B"  
/clone lib="Carp mixed tissue library 2"  
/notes="Vector: pTriplex2; Site 1: SfiI GGCCATTACGGCC;  
Site 2: SfiI GGCGCTCGGC; Normalized and serially  
subtracted cDNA library prepared from mixed tissues of  
warm, cold and hypoxia challenged animals"

# ORIGIN

Alignment Scores:  
Pred. No.: 3,378-39 Length: 844  
Score: 457.50 Matches: 92  
Percent Similarity: 60.43% Conservative: 47  
Best Local Similarity: 40.00% Mismatches: 87  
Query Match: 28.74% Indels: 4  
DB: 14 Gaps: 3

US-10-055-106c-2 (1-305) x CA965628 (1-844)

QY 20 LeuIleSerLeuTyrPheIleValleuIleGlyLeuValGlyValIleSerIleLeu 39  
DB 78 CTTCGTGTTGATATATATATTCATCTTCTTGTGGGACCTCTGAATGTTGACTAATGTC 137  
QY 40 PheLeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 59  
DB 138 TGTATGTACAGTCCCAAGGCGTCTCTTCCACCAAGTGCTGTATCAACCTGATA 197  
QY 60 ValValHisSerVal-PheLeuLeuThrValPropheArgLeuThrTyrLeuIle---Ly 78  
DB 198 GCAGTGCACTCCCTTTCTCTTCACGGTGCCCTTCGATTACTATTATGCTCTAA 257  
QY 78 sLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleH 98  
DB 258 TAAAGACTGGATTCTTGGCATACATTCTGCAAAATTTGTCAGTATATGATCATCCCA 317  
QY 98 sMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePh 118  
DB 318 CATGTATCTTGCAATTAATCTTCTATGCTCTCTTCTTAATGTGCGTATCGGAGCGGTC 377  
QY 118 eLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAalaSerAlaG 138  
DB 378 TGATCAACAACAAGCTAAAGTTTCATCGCATCTTCACGCCACGATTGCAAGTCAAG 437  
QY 138 yMetTrpThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHi 158  
DB 438 CGTCTGGATGTCATATTCGGTGTATGATCCCA---GCNACTGTAATTTGGAATGGC 494  
QY 158 sGluGluTyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVa 178  
DB 495 ACAGAAC---GATTCAACTCATTTGCTTTAATTTTGGTCAGGCTCTACCCAGCGCTACTGT 551  
QY 178 lLysIleIleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuVal 198  
DB 552 GAAGACATTAACTATATTAATTTGTACTANTAACTAGTGTGGAGTGTCTTGGCAGT 611  
QY 198 lPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuSerHi 218  
DB 612 TTTCAGATTATTTTCTGCTCAAGTGAAGTAAACATTTTGGAAAGGCCCATGTCAACG 671

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, UPL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
 UPL: <http://genome.gsc.riken.go.jp/>  
 URL: <http://fantom.gsc.riken.go.jp/>  
 Location/Qualifiers

## COMMENT

## FEATURES

source

1. 2774  
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 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM DB:A530099J19"  
 /db\_xref="MGI:2406345"  
 /db\_xref="taxon:10090"  
 /clone="A530099J19"  
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 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="adult"  
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## CDS

/notes="unnamed protein product; hypothetical  
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 /db\_xref="GI:26334373"  
 /translation="MDVMDVLVNSGVVMPMAEQCDHCRALITAYSVVFFG  
 VGVVMKSHMYLTFYVIAITLRLIYFKLQKQKHAVALSI:IIWTSFIFLP  
 IFLOYGTDPSYEQRCPEFHSLNSRDIIINYSTIVIMTIVLLILLIQMAVLH  
 LKAYMDMAHQBRYRAQIKSPFFLLIVVCFIPHAFRVYFIQNPQENSKLLYN  
 EICVALTAPCLDMLCFIGVH"

## ORIGIN

## Alignment Scores:

Pred. No.: 2,45e-47 Length: 2774  
 Score: 538.50 Matches: 105  
 Percent Similarity: 58.97% Conservative: 66  
 Best Local Similarity: 36.21% Mismatches: 106  
 Query Match: 33.83% Indels: 13  
 DB: 11 Gaps: 4

US-10-055-106C-2 (1-305) x AK041317 (1-2774)

QY 12 CysAspProIleValThrProHisLeuIleSerLeuTyrrPheIleValLeuIleGlyGly 31  
 |||||  
 Db 380 TGTGATGCTACTCTACGACGCAATCTCGACACACCTATAGTGGCTCTTTGGAGGC 439  
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 QY 32 LeuValGlyValIleSerIleLeuPheLeuValIleValIleValIleValIleValThr 51  
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 Db 440 ACCGTTGGACAGTATGATGTCACATGATGTTCAAGAGGAATGCCAATCAATGATT 499  
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 QY 52 ThrMetAlaValIleAsnLeuValValIleHisSerValPheLeuThrValProphe 71  
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 Db 500 GCCACTATCATATATATCATGTGTGACCTCCCTCTCCCTGATGATGTCCTCCATTC 559  
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 QY 72 ArgLeuThrTyrrLeuIleLysLeuThrTrpMetPheGlyLeuPropheCysLysPheVal 91  
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 Db 560 CGGCTCAGTTACTATTTCTACGACGCTCGAAGCTGGGTCTTTTACCTGCCGAATGTT 619  
 |||||  
 QY 92 SerAlaMetLeuHisIleHisMetTyrrLeuThrPheLeuPheTyrrValValIleLeuVal 111  
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 Db 620 AGTGGCGTCATATATGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 679  
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 QY 112 ThrArgTyrrLeuIlePhePheLysCysLysAspLysValGluPheTyrrArgLysLeuHis 131

Db 680 CTTCGGCTGCTCACTATTTTAAG---AACTGCAATGCAACAGTACAAAGTTCCAT 736  
 |||||  
 QY 132 AlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValIleValIleVal 151  
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 Db 737 GCGGTGGCTCTAAGTATTATTATTGGGTGACAGAGCTTCATCTTTTACCATAATTT 796  
 |||||  
 QY 152 ValSerArgTyrrGlyIleHisGluGluTyrrAsnGlu---GluHisCysPheLysPheHis 170  
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 Db 797 TTTTACAAATATGGCAGATCCAGATTATACAGACCAACAGCGGTGCTTGAGTTTCAT 856  
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 QY 171 LysGluLeuAlaTyrrThrTyrrValIleIleAsnTyrrMetIleValIlePheValIle 190  
 |||||  
 Db 857 AAATCTCTCACTCCAGGACATCATCAATAACTATTCTATAATTGTTATTATGATG 916  
 |||||  
 QY 191 AlaValAlaValIleLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLys 210  
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 Db 917 ACAACAGTTCTGCTCTCTTTCTGATACAGATGGCTGTCATCTTCATTTGATAAAGCC 976  
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 QY 211 LeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePhe 230  
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 Db 977 TATTGGCTGATATGTTGGCCCATCAAGATACAGAGCTCAATCAACAGATTTTTCCTC 1036  
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 QY 231 IleGlyValIleLeuValCysPheLeuProTyrrGlnPhePheArgIleTyrrLeuAsn 250  
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 Db 1037 CTGTTGGTCATAGTTGCTCTTATACCCACCATTCAGGCTATATTTTATTCAA 1096  
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 QY 251 ValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrrAsnGluIlePheLeu 270  
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 Db 1097 AATTTTCCAGACCAAGAA-----AATCTAAGTTAATCTGTACAAAGAACTGTGTT 1150  
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 QY 271 SerValThrAlaIleSerCysTyrrAspLeuLeuPheValPheGlyGlySerHis--- 289  
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 Db 1151 GCTTTAACAGCTTCTGCTGCTGATATGTTTTCATAGTGGTGTCTCATCCATTAG 1210  
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 QY 290 -----TrpPhe 291  
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 Db 1211 ACCTTCCCGTGTCTTCTTCTGTGATTGGTTT 1240  
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RG862323 646 bp mRNA linear EST 29-MAY-2001  
 602796201F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',  
 mRNA sequence.  
 RG862323  
 RG862323.1 GI:14212861  
 EST.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
 Plate: LLNL0828 row: b column: 01  
 High quality sequence stop: 644.  
 Location/Qualifiers  
 1. 646  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"

FEATURES  
 source

REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 456)
AUTHORS	Mahairas,G.G., Wallace, J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc.Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
PUBMED	10449764
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics.(info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3162 row: D column: 1 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 456. Location/Qualifiers 1..456 /organism="Homo sapiens" /mol_type="genomic DNA"
FEATURES	source

## ORIGIN

Alignment Scores:	3 148-52	Length:	455
Pred. NO.:		Matches:	128
Score:	574.00	Conservative:	3
Percent Similarity:	82.69%	Mismatches:	22
Best Local Similarity:	80.77%	Indels:	6
Query Match:	36.06%	Gaps:	3
DB:	28		

US-10-055-106C-2 (1-305) X AO888495 (1-456)

Qy	127	TyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValleValle	146
Db	1	TACAGAAACTGCATGCTGTGGCTGCCAGTGTGGACGCTGGTGATGTGCAAT	60
Qy	147	ValValProLeuValValSerArgTyrGlyIleHisGluIuTrpAenGluGluHisCys	166
Db	61	GTGGTACCCCTGGTTGCTCCGGGTATGGAATCATGAGGAATACAAATGAGGAGCACTGT	120
Qy	167	PheLysPheHisLysGluLeuAlaTyrThrTyrValLysIleIleAsnTyrMetIleVal	186
Db	121	TTTAAATTTCACAAAGAGCTTGCTACACATATGTGAAATCATCAACTATATGATAGTC	180
Qy	187	IlePheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetIleu	206
Db	181	ATTNTTGTCTATAGCCGTTGCTGTGATTCGTGTGTCTTCCAGGCTTTCATCATATATGTG	240
Qy	207	MetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLys	226
Db	241	ATGGGTGCAGAACTACGCCACTCTTTACTCCACAGGAGTTCGGGCTCAGCTGANA	300
Qy	227	AsnLeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle	246
Db	301	AAACCTATTTTATAGGGGTTCATCTGTTGTGTTTCTTCCTACCAGT---CTTAGATC	357
Qy	247	TyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsn	266
Db	358	TATTACTTCAATGTGT---GANCATTCCAATGCTGTA---CAGCAGGTGCATTTATACGAA	412

**QY**    267 GlullePhleusSerValThAlalIleSerCysTyAspleuleu 282  
         :::| | | | |  
**DB**    413 -----ATTCTGATGTACACTTACTGTATATTCGTTTGCTT 451

**RESULT 5**

**LOCUS** AK0411317  
**DEFINITION** Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530090719 product:hypothetical Rhodopsin-like GPCR superfamily containing protein, full insert sequence.  
**ACCESSION** AK0411317 GI:26334372  
**VERSION** AK041131.1  
**KEYWORDS** HTC; CAP trapper.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus

**REFERENCE**  
**AUTHORS** Carninci,P. and Hayashizaki,Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**MEDLINE** 99279253  
**PUBMED** 10349636

**REFERENCE**  
**AUTHORS** Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.  
**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)  
**MEDLINE** 20499374  
**PUBMED** 11042159

**REFERENCE**  
**AUTHORS** Shinto,K., Itoch,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi.K., Kitsuai,T., Tashiro,H., Itoh.M., Sumi.N., Ishii.Y., Nakamura.S., Hazama.M., Nishine.T., Harada.A., Yamanoto,R., Matsumoto.H., Sakaguchi.S., Ikegami.T., Hashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawaji,J., Okazaki,Y., Muramatsu.M., Inoue,Y., Kiria,A. and Hayashizaki,Y.  
**TITLE** RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE** 20530913  
**PUBMED** 11076861

**REFERENCE**  
**AUTHORS** The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)

**REFERENCE**  
**AUTHORS** The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

**TITLE** Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
**JOURNAL** Nature 420, 563-573 (2002)

**REFERENCE**  
**AUTHORS** Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno.M., Hanagaki,T., Hara.A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Horii.F., Imotani,K., Ishii,Y., Itoh.M., Kagawa,I., Kasukawa,T., Koita,H., Kawaji.J., Kojima,Y., Kondo,S., Konno.H., Kouda,M., Koya,S., Kurihara.C., Matsuyama.T., Miyazaki.A., Murata.M., Nakamura.M., Nishi.K., Nomura,K., Numazaki.R., Onho.M., Ohsato,N., Okazaki,Y., Saio.R., Satoh.H., Sakai,C., Sakai.K., Sakazume,N., Sano.H., Sasaki.D., Shibata,K., Shinagawa.A., Shiraki,T., Sobabe,Y., Tagami.M., Tagawa.A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru.A., Toya,T., Yasunishi.A., Muramatsu,M. and Hayashizaki,Y.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Db 121 TTCGGCTGGATACCTCATCAAGGACCTGGAC-GTTGATTTACCTTCGCAATTT 179  
Qy 91 ValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPheTyrValValIleLeu 110  
Db 180 GTGAGTGCCATGTTACATATCCATGATACATGATCCATTCCTCTTACGTGGTGTACTA 239  
Qy 111 ValThrArgTyrLeuIlePhePhePhePhePhePhePhePhePhePhePhePhePhe 130  
Db 240 GTCATCAGATACCTCATCTTCTCAAGCGTAGACAGCAAGTAGAATTTCTATGAAATTTG 299  
Qy 131 HisAlaValAlaAlaSerAlaGlyMetTyrThrLeuValIleValIleValIleProLeu 150  
Db 300 CATGCAGTTGTCGCAAGTTCTGCCATGTGGCTTCTGGTGATTTGTTATTTGTCCTT 359  
Qy 151 ValValSerArgTyrGlyIleHisGluGluTyrAsnGluGluHisCysPheLysPheHis 170  
Db 360 GTGTTTCTTCAGTATGGAATAGTAGAAGAACATGAGCAACAGTGTCTTATGATTCAT 419  
Qy 171 LysGluLeuAlaTyrThrTyrValIysIleIleAsnTyrMetIleValIlePheValIle 190  
Db 420 AAGACATCTGGCCATGATCTCTGCGAGTTATCACTACATGATAGTATGTTGTGATA 479  
Qy 191 AlaValAlaValIleLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLys 210  
Db 480 GCTGTGCGTGTGATCTCTTGGGTTTCCAGGTCTTCATCATGTTCCATGTCGGAAG 539  
Qy 211 LeuArgHisSerLeuLeuSerHisGlnGluPheTyrPalaGlnLeuLysAsnLeuPhePhe 230  
Db 540 TTTGGCCATCTCTTACTATC-CACGAGGATCTCTGGGCACAACTGMAAATCTTTCTT 598  
Qy 231 IleGlyValIleLeu---ValCysPheLeuProTyrGlnPhePheArgIle 246  
Db 599 ATAGTATCACTTATCCATTTGGGTTTCTCCCTACCAGTTCCTTCAGGATT 649

RESULT 3  
AZ554824  
LOCUS  
DEFINITION  
RPCI-23-211E13.TV RPCI-23 Mus musculus genomic clone  
RPCI-23-211E13, genomic survey sequence.  
ACCESSION  
AZ554824  
VERSION  
AZ554824.1 GI:11234644  
KEYWORDS  
GSS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 580)  
Zhao,S., Niegman,W., Feldblyum,T., Malek,J., Shatsman,S.,  
Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de  
Jong,P., and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-211E13.TJ  
Contact: Shaving Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
or from Resea ch Genetics (info@resgen.com). BAC end page:  
[http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 211 row: E column: 13  
Seq primer: 17  
Class: BAC ends.  
Location/Qualifiers  
1..580  
/organism="Mus musculus"

FEATURES  
source

/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
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/lab\_host="DH10B"  
/clone\_lib="RPCI-23"  
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:  
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBACe3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."  
ORIGIN  
Alignment Scores: Length: 580  
Pred. No.: 704.00 Matches: 134  
Score: 704.00  
Percent Similarity: 87.43% Conservative: 19  
Best Local Similarity: 76.57% Mismatches: 22  
Query Match: 44.22% Indels: 1  
DB: 28 Gaps: 0  
US-10-055-106C-2 (1-305) x AZ554824 (1-580)  
Qy 130 LeuHisAlaValAlaAlaSerAlaGlyMetTyrThrLeuValIleValIleValIleValPro 149  
Db 3 TTGCATGCAAGTTGCTGCAAGTTCTGC-CGTGGCTCTGCTGATTTGTTGTCGCC 61  
Qy 150 LeuValValSerArgTyrGlyIleHisGluGluTyrAsnGluGluHisCysPheLysPhe 169  
Db 62 TTGCTGTTTCTCAGTATGGAATAGTAGAAGAACATGAGCAACAGTGTCTTATGATTC 121  
Qy 170 HisLysGluLeuAlaTyrThrTyrValIysIleIleAsnTyrMetIleValIlePheVal 189  
Db 122 CATAAAGAACTTGGCCATGATCTGTGCGAGTTATCACTATATGATGATGTTGTC 181  
Qy 190 IleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMetValGln 209  
Db 182 ATAGCTGTTGCGTGTGATTTCTTGGGTTTCCAGGTTTTCATCATTGTCATGGTGGCG 241  
Qy 210 LysLeuArgHisSerLeuLeuSerHisGlnGluPheTyrPalaGlnLeuLysAsnLeuPhe 229  
Db 242 AAGTTTGGCCATCTCTTACTATCCACAGGAGTTCTGGGCACAACTGMAAATCTTTTC 301  
Qy 230 PheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyrTyrLeu 249  
Db 302 TTTATAGTATCATATTATTATTTTCTTCCCTACCAGTTCTTCCAGGATTTATTACTTG 361  
Qy 250 AsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluIlePhe 269  
Db 362 TATGTTGGCCATCTCCAGAGCTGTAAACAAAGTTGCATTTTACATGAAATCTTA 421  
Qy 270 LeuSerValThrAlaIleSerCysTyrAspLeuLeuLeuPheValPheGlyGlySerHis 289  
Db 422 TTGAGCACAAACAGCCATCAGTGTCTGATTTGCTGCTTTTCTTCTTGGAGAGCCAT 481  
Qy 290 TTPPheLysGlnLysIleIleGlyLeuTyrAsnValLeuLeuCys 304  
Db 482 TGGGTTAAGCAAAAGATTTGTCGACATGTCGATTTGCTTATGTC 526  
RESULT 4  
AQ888495  
LOCUS  
DEFINITION  
HS 3162\_B1\_B01.MR CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey  
sequence.  
ACCESSION  
AQ888495  
VERSION  
AQ888495.1 GI:6344685  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toraki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE BAC end sequences of Library RPI-43  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 684)  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toraki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpansegsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 COMMENT Clones are derived from the chimpanzee BAC library RPI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.  
 PRIMERS  
 Sequencing: TU  
 LIBRARY  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI  
 Location/Qualifiers  
 1. 684  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="RP43-007G22.TU"  
 /sex="male"  
 /cell\_type="lymphocytes"  
 /clone\_lib="RPI-43 Chimpanzee Male BAC Library"

FEATURES  
 source  
 1. 29e-91 Length: 684  
 938.00 Matches: 179  
 Percent Similarity: 96.76% Conservative: 0  
 Best Local Similarity: 96.76% Mismatches: 6  
 Query Match: 58.92% Indels: 0  
 DB: 29 Gaps: 0

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.29e-91 Length: 684  
 Score: 938.00 Matches: 179  
 Percent Similarity: 96.76% Conservative: 0  
 Best Local Similarity: 96.76% Mismatches: 6  
 Query Match: 58.92% Indels: 0  
 DB: 29 Gaps: 0

US-10-055-106c-2 (1-305) x AG145972 (1-684)  
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerLagLysMetThr 140  
 Db 10 AAAAAATCCGCGCTTTCTACAGAAATGTCATGCTGCTGCCAGTCTGCCATGG 69  
 QY 141 ThrLeuValLeuValLeuValProLeuValValSerArgTyrGlyHisGluGlu 160  
 Db 70 ACGCTGTGTATGCTATGTTGGTACCCCTGTTGTCTCCCGGATGGAATCCATGAGAA 129  
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  
 Db 130 TACATGAGAGAGACATGTTTACATTTACAAAGAGCTTGTACACATATGTGAAATC 189  
 QY 181 IleAsnTyrMetLeuValLeuPheValIleAlaValAlaValLeuLeuValPheGln 200  
 Db 190 ATCAACTATATGATGATGATTTTGTATGATGATGATGATGATGATGATGATGATG 249  
 QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220  
 Db 250 GTCTTCATCATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 309  
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValLeuValCysPheLeuPro 240  
 Db 310 TTCTGGGCTCAGCTGAAACCTATTTTATATGAGGCTCATCTCTGTTGTTGTTGTTG 369  
 QY 241 TyrClnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260  
 Db 370 TACAGTTCTTTAGATCTATTTACTTGAATGTTGACGATTTCCATGCTGCTAACAG 429  
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280

Db 430 AAGTTTCATTTTATAACGAAATCTTCTGAGCTGTAAACAGCAATTAGCTGCTATGATTG 489  
 QY 281 LeuLeuPheValPheGlySerHisTrpPheLysGlnLysValIleGlyLeuThrPhe 300  
 Db 490 CTTCTCTTTGCTTTTGGGGAGCCATGCTGTTAAACGAAAGATATATGACTTAAGGAAT 549  
 QY 301 CysValLeuCysArg 305  
 Db 550 TGAGTTTGTGCGGT 564

RESULT 2  
 BF160725 772 bp mRNA linear EST 30-OCT-2000  
 LOCUS 601769127F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF160725  
 VERSION BF160725.1 GI:11040832  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 772)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-x@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM9196 row: f column: 07  
 High quality sequence stop: 634.  
 Location/Qualifiers  
 1. 772  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="Czech II"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3988230"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin.  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Lu29"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Library constructed by Life Technologies. Investigator  
 Providing samples: Gilbert Smith, NIH"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.27e-81 Length: 772  
 Score: 844.50 Matches: 177  
 Percent Similarity: 88.02% Conservative: 14  
 Best Local Similarity: 81.57% Mismatches: 25  
 Query Match: 53.05% Indels: 3  
 DB: 10 Gaps: 1

US-10-055-106c-2 (1-305) x BF160725 (1-772)  
 QY 31 GlyLeuValGlyValIleSerIleLeuPheLeuValLysMetAsnThrArgSerVal 50  
 Db 1 GGACTGGTAGGCTCATCTCCATCTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTG 60  
 QY 51 ThrThrMetAlaValIleAsnLeuValValHisSerValPheLeuLeuThrValPro 70  
 Db 61 ACCACCATGGTGTCTCATCACTGGTGGTGGTTCATGGGTCTCTCTACTACGGTGGCT 120  
 QY 71 PheArgLeuThrTyrTyrLeuIleLysLysThrTrpMetPheGlyLeuProPheCysLysPhe 90

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 25, 2004, 19:56:50 ; Search time 2904 Seconds  
(without alignments)  
3136.352 Million cell updates/sec

Title: US-10-055-106C-2  
Perfect score: 1592  
Sequence: 1 MPQHNTSRNSSCDPIVTPHL.....GGSHWFKQKIIGLWNCVLCR 305

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10055106/runat\_21042004\_161131\_26191/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOP=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HAPSPZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10055106@cgn\_1\_1\_2810 @runat\_21042004\_161131\_26191 -NCPU=6 -ICPU=3  
-NO MAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_nam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_ptg.\*
- 27: em\_gss\_vrl.\*
- 28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	938	58.9	684	29	AG145972	AG145972 Pan trogl
2	844.5	53.0	772	10	BF160725	BF160725 601769127
3	704	44.2	580	28	A2554824	A2554824 RPTC-23-2
4	574	36.1	456	28	AQ888495	AQ888495 HS 3162 B
5	538.5	33.8	2774	11	AK041317	AK041317 Mus muscu
6	494	31.0	646	12	BG862323	BG862323 602796201
7	457.5	28.7	844	14	CA965628	CA965628 CCLX05A15
8	369	23.2	834	9	AJ455645	AJ455645 AU455645
9	368.5	23.1	680	14	CA355790	CA355790 627748 NC
10	356	22.4	649	12	BG461295	BG461295 RST44080
11	328	20.6	679	14	CD469227	CD469227 LeukOS2.2
12	324	19.7	499	14	CD698779	CD698779 EST16303
13	305	19.2	478	12	BG145683	BG145683 mac33C07
14	288.5	18.1	733	13	CA050323	CA050323 ssalr9B52
15	261	16.4	648	14	CB514250	CB514250 ssalr9B54
16	249	15.6	283	12	BG221739	BG221739 RST41554
17	241.5	15.2	2755	11	AK033476	AK033476 Mus muscu
18	236.5	14.9	1081	29	AY406930	AY406930 Pan trogl
19	236	14.8	1149	29	AY406931	AY406931 Mus muscu
20	235	14.8	1856	11	AK039528	AK039528 Mus muscu
21	231.5	14.5	1146	29	AY406929	AY406929 Homo sapi
22	231.5	14.5	1199	11	AF345566	AF345566 Homo sapi
23	229.5	14.4	1878	11	AK033675	AK033675 Mus muscu
24	228	14.3	1819	11	AK039041	AK039041 Mus muscu
25	225.5	14.2	1014	29	AY404081	AY404081 Mus muscu
26	218	13.7	1176	29	AY400827	AY400827 Homo sapi
27	218	13.7	1176	29	AY400829	AY400829 Mus muscu
28	218	13.7	2014	11	AK046464	AK046464 Mus muscu
29	217	13.6	1002	29	AY406923	AY406923 Homo sapi
30	217	13.6	1258	11	AF345567	AF345567 Homo sapi
31	217	13.6	1990	11	BC040850	BC040850 Homo sapi
32	217	13.6	2938	11	BC045651	BC045651 Homo sapi
33	215	13.5	996	29	AY401365	AY401365 Homo sapi
34	215	13.5	996	29	AY401366	AY401366 Pan trogl
35	214.5	13.5	1501	11	AK080394	AK080394 Mus muscu
36	214	13.4	834	29	CS586141	CS586141 CH240_383
37	211.5	13.3	996	29	AY401267	AY401267 Mus muscu
38	211	13.3	1062	29	AY400424	AY400424 Mus muscu
39	210.5	13.2	1687	11	AK039791	AK039791 Mus muscu
40	210	13.2	987	29	AY401371	AY401371 Homo sapi
41	210	13.2	2724	11	BC033445	BC033445 Homo sapi
42	208.5	13.1	1008	29	AY406925	AY406925 Mus muscu
43	208	13.1	2708	11	AK076275	AK076275 Mus muscu
44	207.5	13.0	814	29	AY405237	AY405237 Homo sapi
45	207.5	13.0	960	29	AY409037	AY409037 Mus muscu

ALIGNMENTS

RESULT 1  
AG145972  
LOCUS  
DEFINITION AG145972 684 bp DNA linear GSS 08-JAN-2002  
Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey  
sequence.  
ACCESSION AG145972  
VERSION AG145972.1 GI:16675650  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1